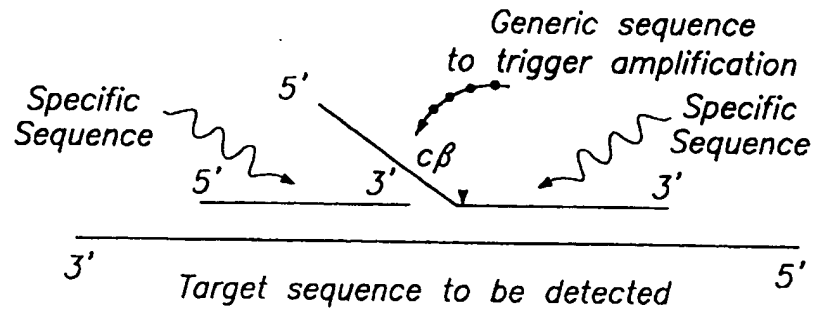
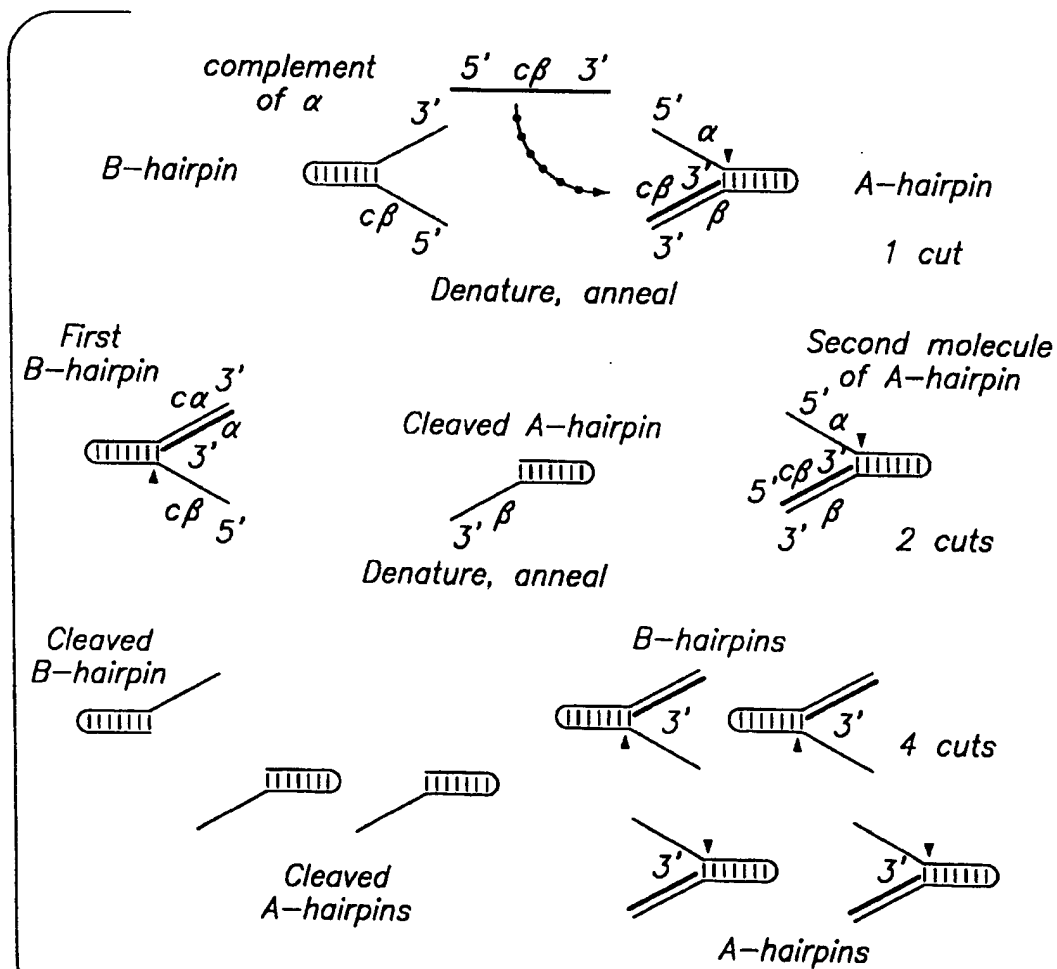


FIG. 1A



**FIG. 1B** PART ONE: TRIGGER REACTION



**FIG. 1C** PART TWO: DETECTION REACTION

1007429, 061202

1007429, 061202

**FIG. 2B**

MAJORITY	[SEQ ID NO:7]	CGAGCGGAGGAGGTXCTGGCCACCTGGCCAAAGAGCGGAAAGGAGGGGTACGAGGTCGGCATCCTC
DNAPTAQ	[SEQ ID NO:1]	.....C.....G.....C.....C.....417
DNAPTFL	[SEQ ID NO:2]	T.....G.....CG.....C.....414
DNAPTTH	[SEQ ID NO:3]	.....T..C.....C.....C.....420
MAJORITY		ACGGCGGACGGGACCTCTACGAGCTCCTTCGGACCGCATCGCGGTCTCCACCCGAGGGGTACCTCA
DNAPTAQ		.....AAA.....T.....CA.....487
DNAPTFL		T.....T.....G..G.....A.....T.....G..484
DNAPTTH		.....A.....A..G.C.....G.....CC.....490
MAJORITY		TCACCCGGCGGTGGCTTTGGGAGAGTACGGCCTGAGCGCGGAGCACTGGGTGGACTACCGGGCCCTGGC
DNAPTAQ		.....C.....A.....A.....C..C.....CC.....A..557
DNAPTFL		.....AC.....C.C.....C.....C.....554
DNAPTTH		.....A.....C.....C.....T...C.....C..T..560
MAJORITY		GGGGGACCCCTCCGACAACCTCCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCXGAAGCTCCTCXAG
DNAPTAQ		C.....CAG.....T.....G..GAG.....T..GG..627
DNAPTFL		.....G..T..A.....G.....A..G...A..CGC..624
DNAPTTH		.....A.....TC.....TC.....A..630
MAJORITY		GAGTGGGGGAGCCTGGAAACCTCCTCAAGAACCTGGACCGGGTGAGGCCCGC...CXTCCGGGAGAGA
DNAPTAQ		.....GC.....C.....A.....A.....694
DNAPTFL		.....T..C..C.....A.....T...T..G.....C..691
DNAPTTH		.....A.....A.....A.....A.AAA..G.....700



FIG. 2D

MAJORITY [SEQ ID NO:73]	CGGGGCTGCTGGCCAAAGGACCTGGCCGTTTGGCCCTGAGGGAGGGCCCTXGACCTCXTGCCCGGGGACG	1174
DNAPTAD [SEQ ID NO:1]	.....G..T.....A.....AG.....C.....A.....T..G....CC.....C.....	1181
DNAPTFL [SEQ ID NO:2]	.....AA.....G.....G.....C.....G.....T..C..A..A.....	1190
DNAPTTH [SEQ ID NO:3]	.....C.....C.....C.....TC.....G..A.....G.....	
MAJORITY	ACCCCATGCTGCTGGCCTAGCTGCTGGACCCCTCCAACACCCGCGGAGGGGCTGGCCCGCGCTACGG	
DNAPTAD	.....T.....T.....	1184
DNAPTFL	.....G.....T.....T.....T.....	1181
DNAPTTH	.....G.....G.....	1190
MAJORITY	GGGGGAGTGGACGGAGGAXGGGGGGGAGCGGGCCCTCCTXICCGAGAGGGCTCTTCCXGAACCTXXXGGAG	
DNAPTAD	C.....G.....G.....GC...T.....GCC.....GTG..G..	1254
DNAPTFL	.....T.....A.....GG.....C..G.....A..C...AAA....	1251
DNAPTTH	.....G..C.CCC.C.....C..G.....CAT..G.....CCTTA..	1260
MAJORITY	CGCCTTGAGGGGAGGAGGGCTCCTTTGGCTTTACGAGGAGGTGGAGAAAGCCGCTTTCGGGGGTCCCTGG	
DNAPTAD	A..G.....G.....G.....G.....GCT.....	1324
DNAPTFL	.....A..A..A..AC..C..G.....G.....G.....GT...	1321
DNAPTTH	.....C.....A.....C.....C.....A.....C.....	1330
MAJORITY	CCCACATGGAGGGCCACGGGGCTXCGGCTGGACGTGGCCCTACCTCCAGGGCCGCTXTCCTGGAGGTTGGCGGA	
DNAPTAD	.....G..C.....G..C.....T...AG....T..G.....C..	1394
DNAPTFL	GG.....C.....C.....T.....C.....A..G	1391
DNAPTTH	.....C.....C.....A.....T.....T.....C..T.....	1400

# FIG. 2E

MAJORITY [SEQ ID NO:7]	GGAGATCGGCGCGCTCGAGGAGGAGGCTCTTCGGGCTGGCCGGGACCCGCTTCAACCTCAACTCCCGGGAC	1464
DNAPTAA [SEQ ID NO:1]	.....GC.....CC.....	1461
DNAPTFL [SEQ ID NO:2]	...G.G...AG..G.....	1470
DNAPTTH [SEQ ID NO:3]	.....T.....G.....	
MAJORITY	CAOCTGGAAGCGTCTCTTGCAGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAGACXGCCAAGC	
DNAPTAA	.....C.....A.....	1534
DNAPTFL	...GC.....G..C..G..T.....	1531
DNAPTTH	.....TA.....T.G..G.....C.A.....A.....	1540
MAJORITY	GCTCCAGCAGCGCGCGCTGCTGGAGCGGCTXCGXGAGGGCGGACCGCCATCGTGGAGAGATCCTGCCAGTA	
DNAPTAA	.....C.....C..C.....	1604
DNAPTFL	.....T.....G..A.....CCGC.....	1601
DNAPTTH	.....G.....A..G.....C...C..	1610
MAJORITY	CCGGGAGGCTCACCAGGCTCAAGAACACACCTACATXGACCGCGCTGCCXGXCGCTCGTCCACCCGAGGACGGGC	
DNAPTAA	.....G.....G.....T.....G.A...A.....	1674
DNAPTFL	.....A.....C.C...G.....A...C...C...	1671
DNAPTTH	.....G.G.....G..AAG.....G.....	1680
MAJORITY	CGCCTCCACACCGCGCTTCAACCAGACGGCGGCGGCGGAGGCTTAGCTCCGACCCCAACCTGC	
DNAPTAA	.....A.....T.....C..	1744
DNAPTFL	..G.....C.....TCC.....	1741
DNAPTTH	.....G.....	1750

FIG. 2F

MAJORITY [SEQ ID NO:71]	AGAACATCCCGCTCCGCACCCXCTGGCCAGAGGATCCGCCCGGCCCTTCGTGGCCGAGGAGGGGTGGGT	
DNAPTAA [SEQ ID NO:1]	.....G..T..G.....A..C.....G....C..	1814
DNAPTFL [SEQ ID NO:2]	.....G.....T.....C..C.....A.....C.....	1811
DNAPTTH [SEQ ID NO:3]	.....CT.....C.....C.....T.....C.....	1820
MAJORITY	GTGGTGGCCCTGGACTATAGGCAGATAGAGCTCCGGGTCTGGCCCACTCTCCGGGGACGAGAACCTG	
DNAPTAA	A.....A.....A.....G.....C.....	1884
DNAPTFL	.....T..T.....C.....T.....T.....C.....	1881
DNAPTTH	.....A.....A.....C.....C.....A.....	1890
MAJORITY	ATCCGGGTCTTCCAGGAGGGAGGACATCCACACCCAGACCGCCAGCTGGATCTTCGGCCCTCCCGCCGG	
DNAPTAA	.....C.....C.....GG.....G....G...	1954
DNAPTFL	.....T.....T.....T.....TT....C..	1951
DNAPTTH	.....A.....A.....A.....A.....	1960
MAJORITY	AGGCCGTGGACCCCTGATGCCGCCGGCGGCCCAAGACCATCAACTTCGGGGTGGTCTAGGGCATGTCCCG	
DNAPTAA	.....A.....A.....A.....A.....G....	2024
DNAPTFL	.....A..G..A.....T.....GG..G.....G.....	2021
DNAPTTH	.....A.....A.....A.....A.....C.....	2030
MAJORITY	CCACCGCCCTCTCCAGGAGCTTGGCATCCGCTACGAGGAGGGGGTGGCCCTTCATTGAGGGCTACTTCCAG	
DNAPTAA	.....A.....A.....T.....CCA.....T...	2094
DNAPTFL	.....GG.....T.....T.....T.....	2091
DNAPTTH	.....TA.G.....A.....T..A.....A	2100

1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100



100-42265-554202

2304  
2301  
2310

FIG. 2H

MAJORITY [SEQ ID NO:7]	GGCCCTGGAGGTGGAGGTGGGATGGGGAGGACTGGCTCTCGGCCAAGGAGTAG
DNAPTAA [SEQ ID NO:1]	.....A..... GA
DNAPTFL [SEQ ID NO:2]	.....CC.....
DNAPTTH [SEQ ID NO:3]	.....T..... GT...

100-4328-05242



FIG. 3B

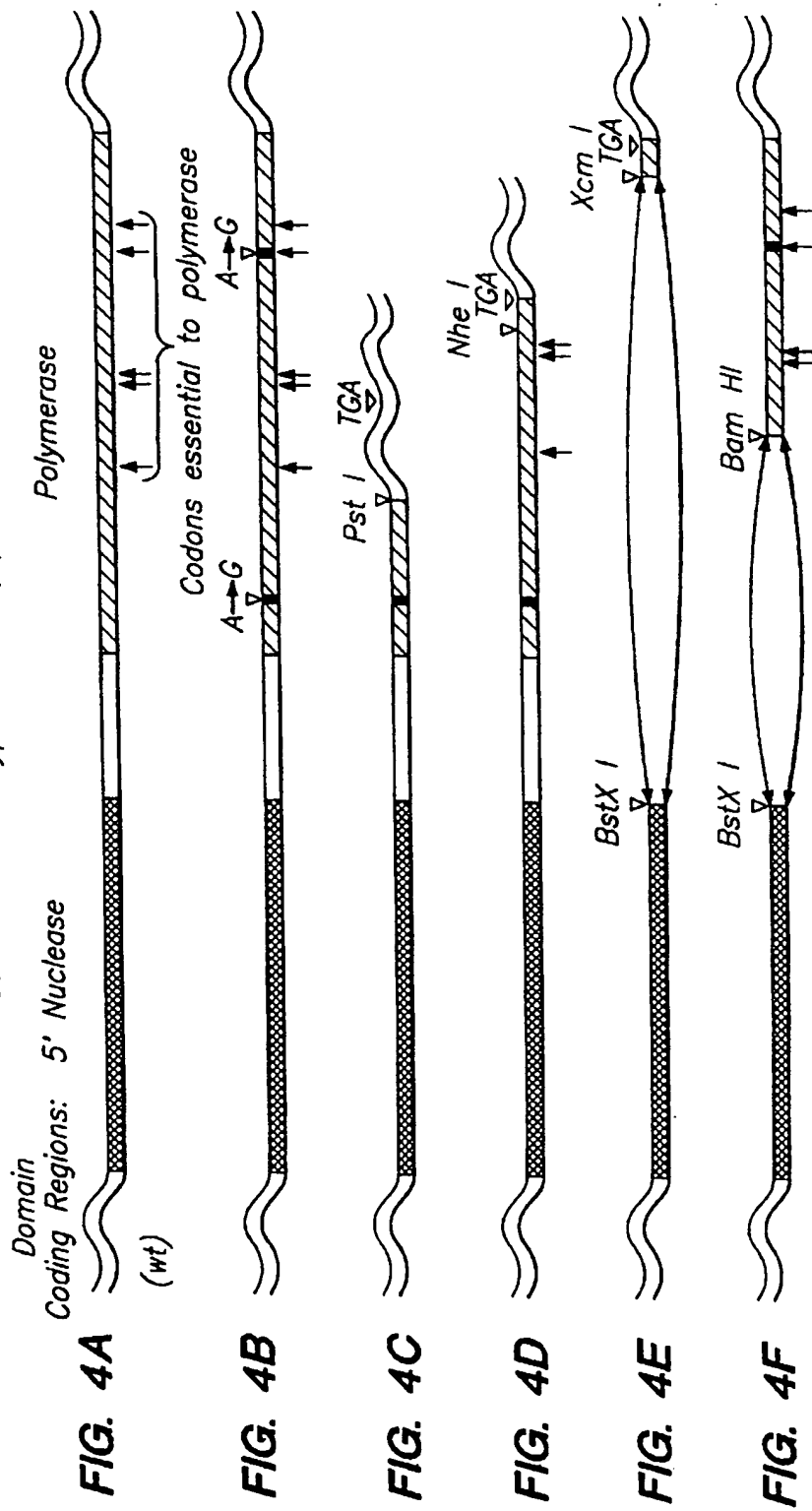
MAJORITY [SEQ ID NO:8]	RGLLAKOLAVLALREGLDLXPDDPMLLAYLLDPSNTTPEGVARRYGGEWTEADAGERALLSERLFXNLXX	
TAQ PRO [SEQ ID NO:4]	S.....G.P.....E.....A.....A.....WG	418
TFL PRO [SEQ ID NO:5]	I.....F.E.....A.....QT.KE	417
TTH PRO [SEQ ID NO:6]	S.....V.....AH.....HR..LK	420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEI RRLEEEVFRLAGHPFNLNSRD	
TAQ PRO	R...R...A.....R.....A.....A.....	488
TFL PRO	K.....E.....R.....EA.V.Q.....	487
TTH PRO	K.....H.....L.....	490
MAJORITY	OLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKNTYIDPLPLVHPRTG	
TAQ PRO	.....S.....D.I.....	558
TFL PRO	.....DR.....A.....K..	557
TTH PRO	R...L...Q.....H.....V....S.....	560
MAJORITY	RLHTRFNOTATATGRSSSDPNLQNI PVRTPIGQRI RRAFFVAEEGWXLVALDYSOIELRVLAHLSGDENL	
TAQ PRO	.....L.....L.....	628
TFL PRO	.....V...V.....	627
TTH PRO	.....A..A.....	630
MAJORITY	IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHLRSQELAI PYEEAVAFIERYFO	
TAQ PRO	.....E.....R.....Q.....	698
TFL PRO	.....S.G.....G..S.....	697
TTH PRO	K.....V.....	700

10074322 . 061402

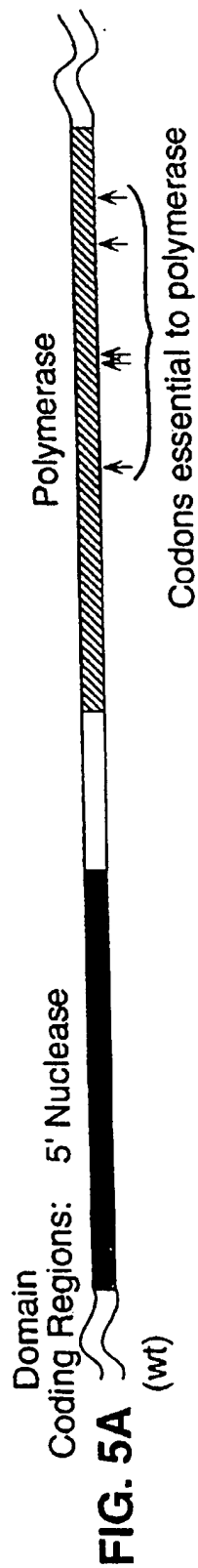
• • •

1  
 2  
 3  
 4  
 5  
 6  
 7  
 8  
 9  
 10  
 11  
 12  
 13  
 14  
 15  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25  
 26  
 27  
 28  
 29  
 30  
 31  
 32  
 33  
 34  
 35  
 36  
 37  
 38  
 39  
 40  
 41  
 42  
 43  
 44  
 45  
 46  
 47  
 48  
 49  
 50  
 51  
 52  
 53  
 54  
 55  
 56  
 57  
 58  
 59  
 60  
 61  
 62  
 63  
 64  
 65  
 66  
 67  
 68  
 69  
 70  
 71  
 72  
 73  
 74  
 75  
 76  
 77  
 78  
 79  
 80  
 81  
 82  
 83  
 84  
 85  
 86  
 87  
 88  
 89  
 90  
 91  
 92  
 93  
 94  
 95  
 96  
 97  
 98  
 99  
 100  
 101  
 102  
 103  
 104  
 105  
 106  
 107  
 108  
 109  
 110  
 111  
 112  
 113  
 114  
 115  
 116  
 117  
 118  
 119  
 120  
 121  
 122  
 123  
 124  
 125  
 126  
 127  
 128  
 129  
 130  
 131  
 132  
 133  
 134  
 135  
 136  
 137  
 138  
 139  
 140  
 141  
 142  
 143  
 144  
 145  
 146  
 147  
 148  
 149  
 150  
 151  
 152  
 153  
 154  
 155  
 156  
 157  
 158  
 159  
 160  
 161  
 162  
 163  
 164  
 165  
 166  
 167  
 168  
 169  
 170  
 171  
 172  
 173  
 174  
 175  
 176  
 177  
 178  
 179  
 180  
 181  
 182  
 183  
 184  
 185  
 186  
 187  
 188  
 189  
 190  
 191  
 192  
 193  
 194  
 195  
 196  
 197  
 198  
 199  
 200  
 201  
 202  
 203  
 204  
 205  
 206  
 207  
 208  
 209  
 210  
 211  
 212  
 213  
 214  
 215  
 216  
 217  
 218  
 219  
 220  
 221  
 222  
 223  
 224  
 225  
 226  
 227  
 228  
 229  
 230  
 231  
 232  
 233  
 234  
 235  
 236  
 237  
 238  
 239  
 240  
 241  
 242  
 243  
 244  
 245  
 246  
 247  
 248  
 249  
 250  
 251  
 252  
 253  
 254  
 255  
 256  
 257  
 258  
 259  
 260  
 261  
 262  
 263  
 264  
 265  
 266  
 267  
 268  
 269  
 270  
 271  
 272  
 273  
 274  
 275  
 276  
 277  
 278  
 279  
 280  
 281  
 282  
 283  
 284  
 285  
 286  
 287  
 288  
 289  
 290  
 291  
 292  
 293  
 294  
 295  
 296  
 297  
 298  
 299  
 300  
 301  
 302  
 303  
 304  
 305  
 306  
 307  
 308  
 309  
 310  
 311  
 312  
 313  
 314  
 315  
 316  
 317  
 318  
 319  
 320  
 321  
 322  
 323  
 324  
 325  
 326  
 327  
 328  
 329  
 330  
 331  
 332  
 333  
 334  
 335  
 336  
 337  
 338  
 339  
 340  
 341  
 342  
 343  
 344  
 345  
 346  
 347  
 348  
 349  
 350  
 351  
 352  
 353  
 354  
 355  
 356  
 357  
 358  
 359  
 360  
 361  
 362  
 363  
 364  
 365  
 366  
 367  
 368  
 369  
 370  
 371  
 372  
 373  
 374  
 375  
 376  
 377  
 378  
 379  
 380  
 381  
 382  
 383  
 384  
 385  
 386  
 387  
 388  
 389  
 390  
 391  
 392  
 393  
 394  
 395  
 396  
 397  
 398  
 399  
 400  
 401  
 402  
 403  
 404  
 405  
 406  
 407  
 408  
 409  
 410  
 411  
 412  
 413  
 414  
 415  
 416  
 417  
 418  
 419  
 420  
 421  
 422  
 423  
 424  
 425  
 426  
 427  
 428  
 429  
 430  
 431  
 432  
 433  
 434  
 435  
 436  
 437  
 438  
 439  
 440  
 441  
 442  
 443  
 444  
 445  
 446  
 447  
 448  
 449  
 450  
 451  
 452  
 453  
 454  
 455  
 456  
 457  
 458  
 459  
 460  
 461  
 462  
 463  
 464  
 465  
 466  
 467  
 468  
 469  
 470  
 471  
 472  
 473  
 474  
 475  
 476  
 477  
 478  
 479  
 480  
 481  
 482  
 483  
 484  
 485  
 486  
 487  
 488  
 489  
 490  
 491  
 492  
 493  
 494  
 495  
 496  
 497  
 498  
 499  
 500  
 501  
 502  
 503  
 504  
 505  
 506  
 507  
 508  
 509  
 510  
 511  
 512  
 513  
 514  
 515  
 516  
 517  
 518  
 519  
 520  
 521  
 522  
 523  
 524  
 525

Genes for Wild-Type and Pol(-)DNAPTaq



# Genes for Wild-Type and Pol(-) DNAPTfI



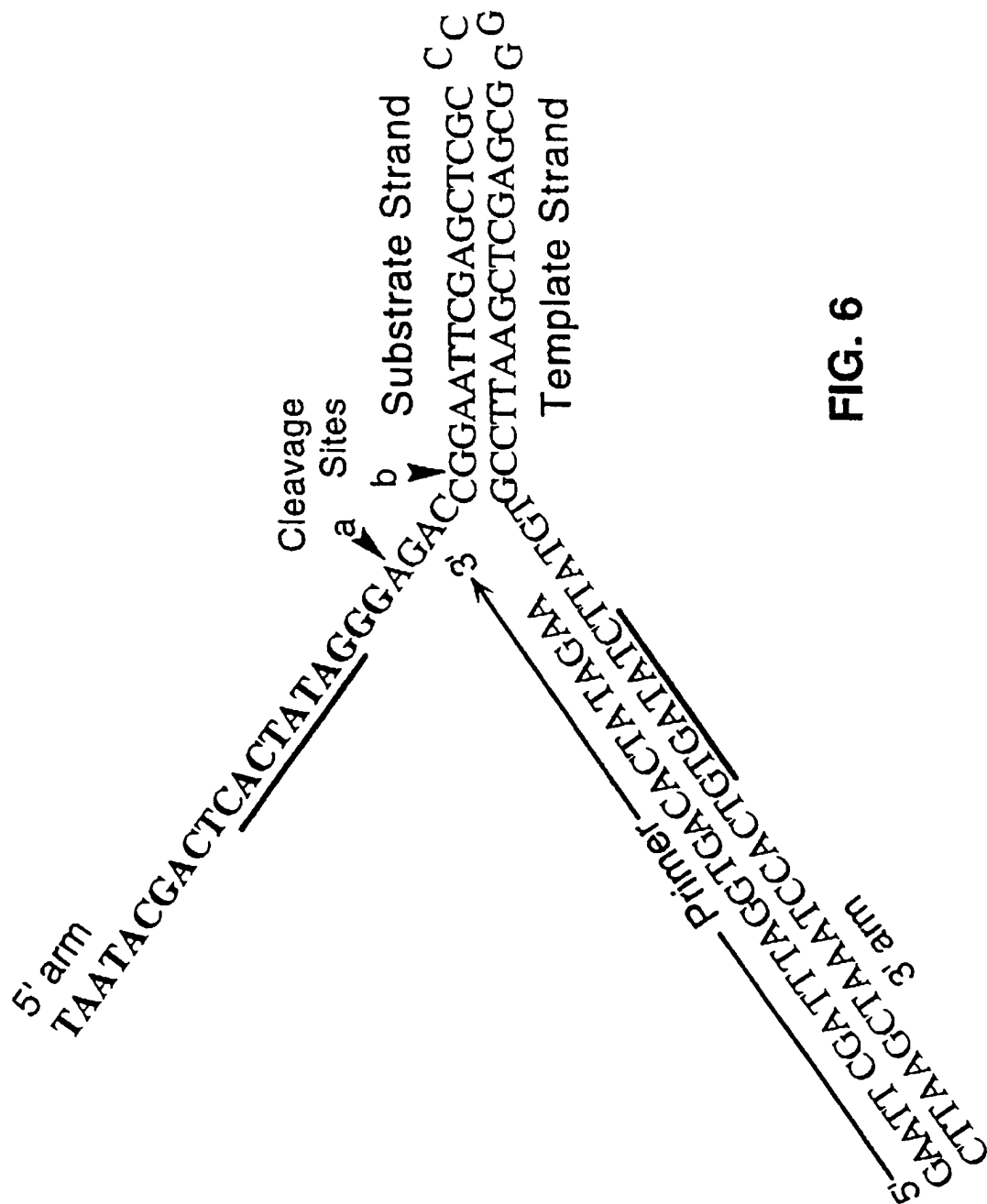
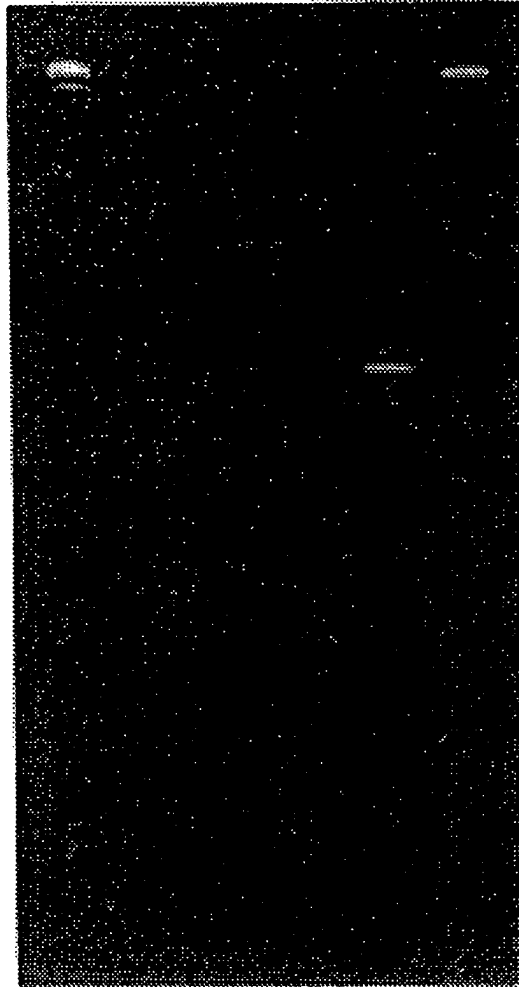


FIG. 6

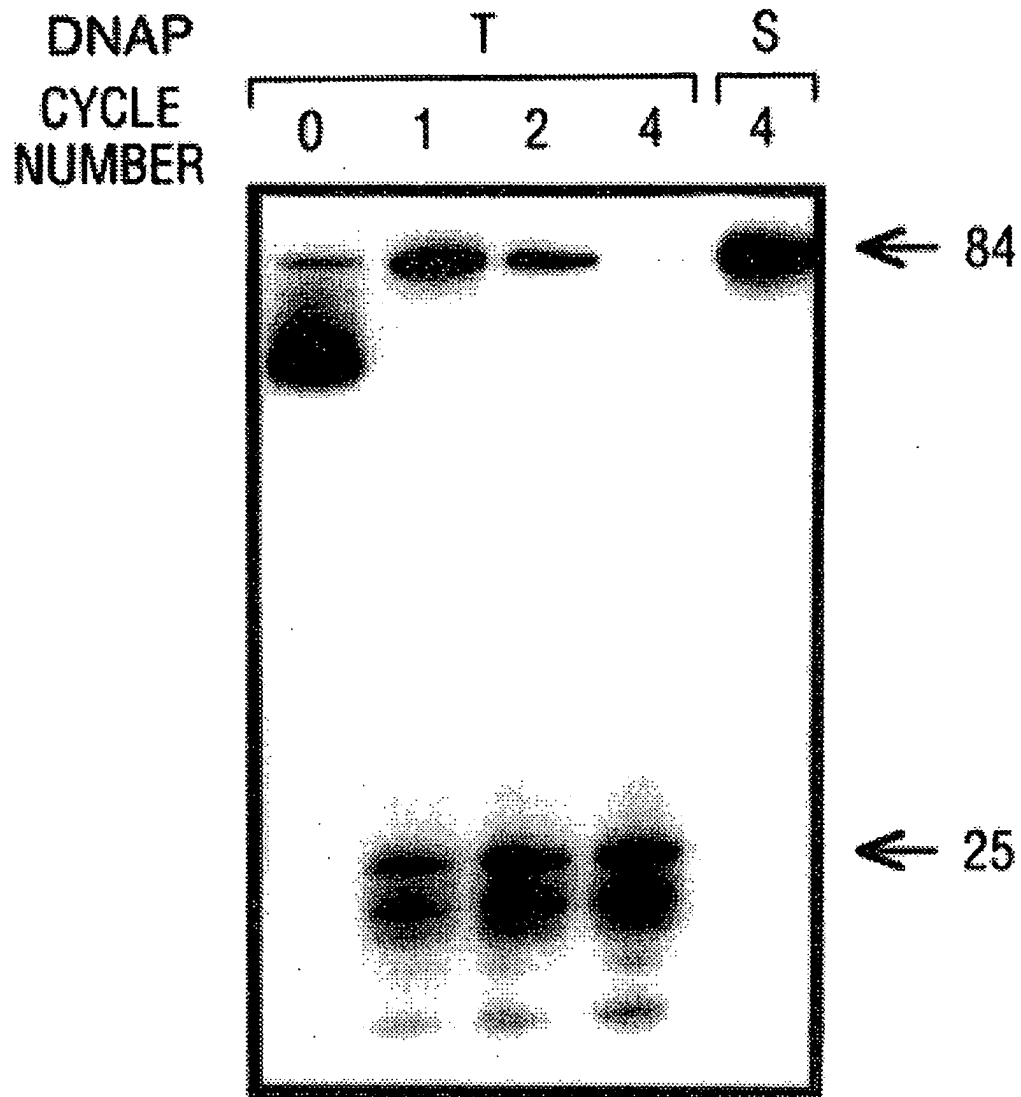


DNAP  
TARGET  
DNA

	T		S		
	-	+	-	+	
M					M



**FIG. 7**

**FIG. 8**

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

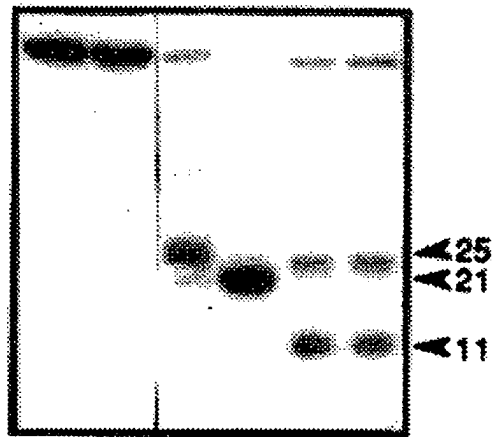


FIG. 9A

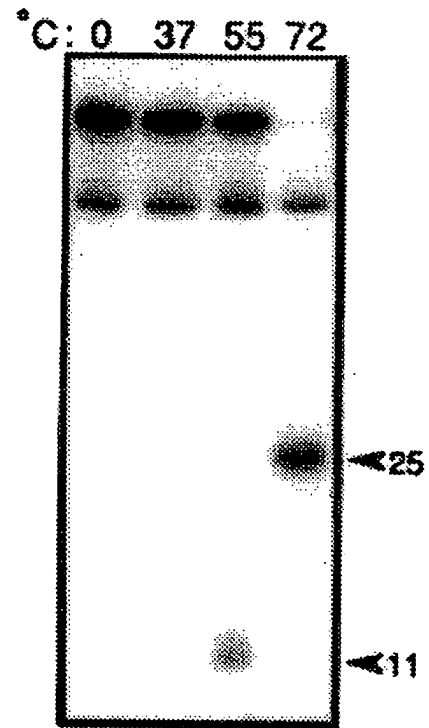


FIG. 9B

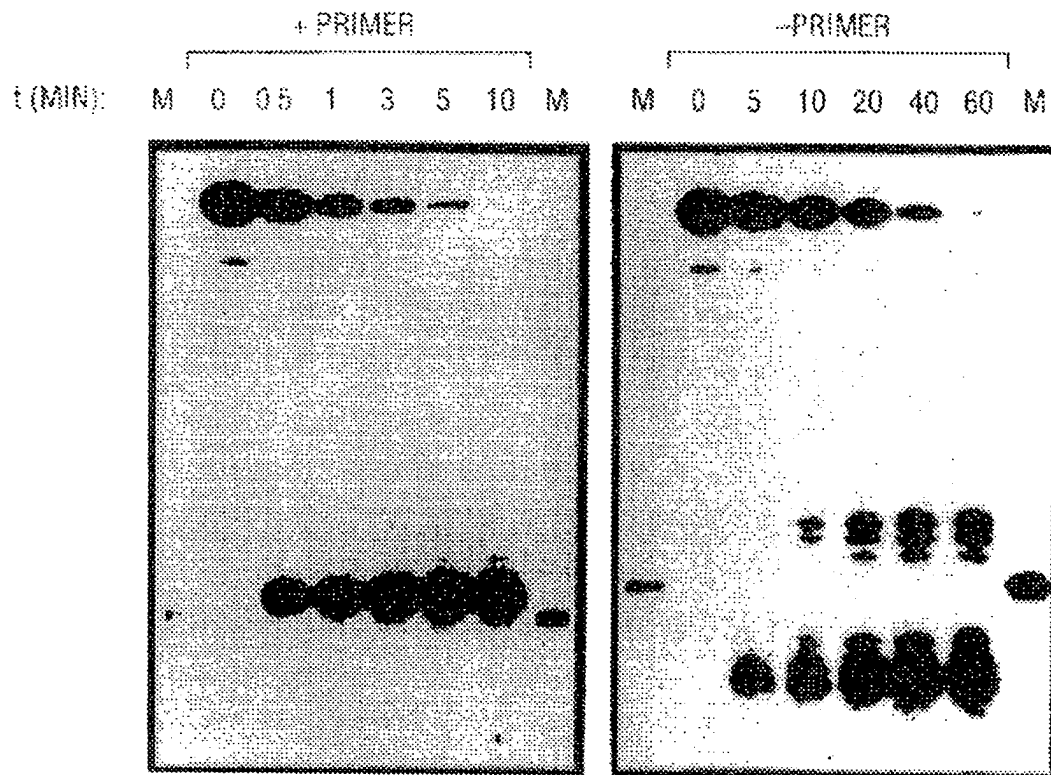


FIG. 10A

FIG. 10B

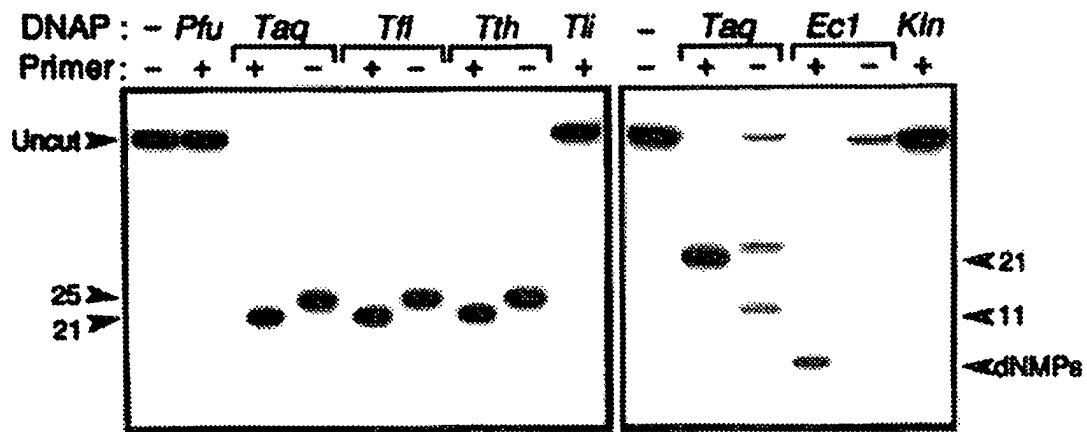
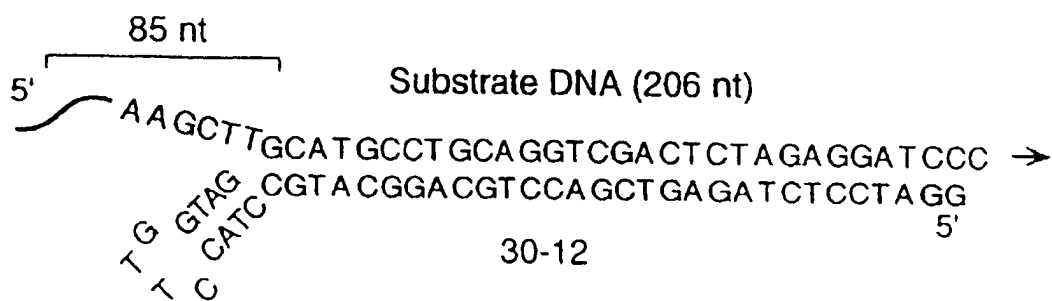
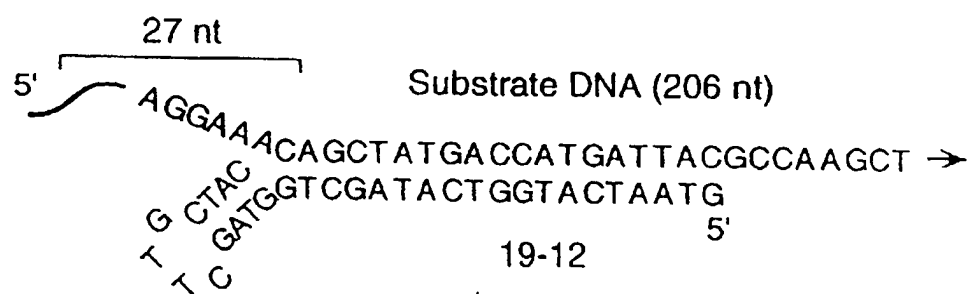
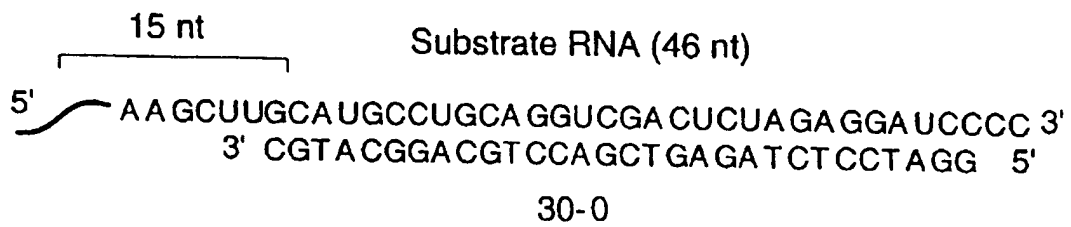


FIG. 11A

FIG. 11B

FIG. 12A



**FIG. 13A**

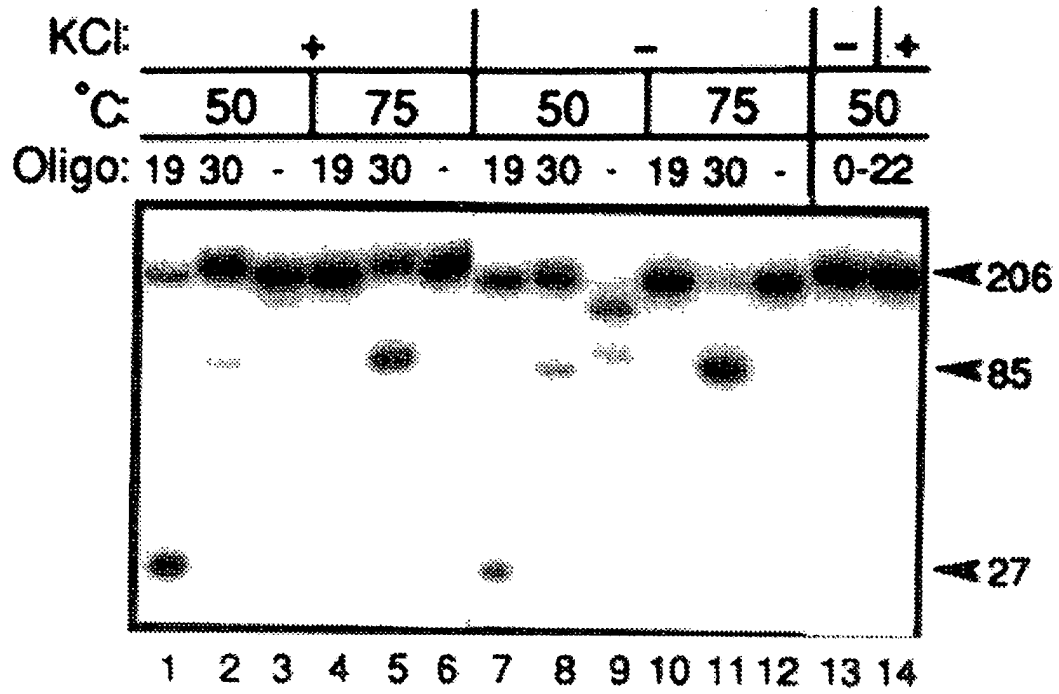


FIG. 12B

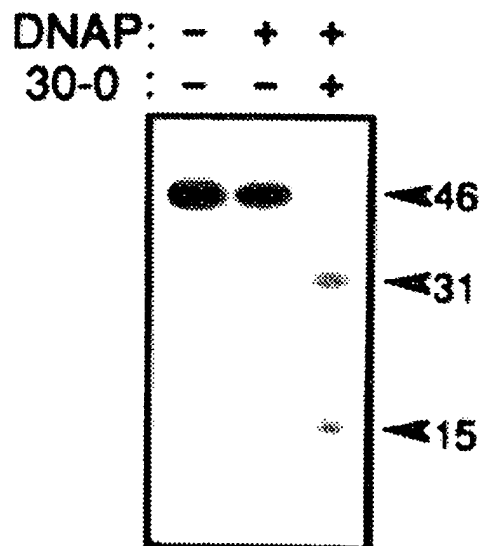
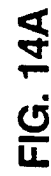


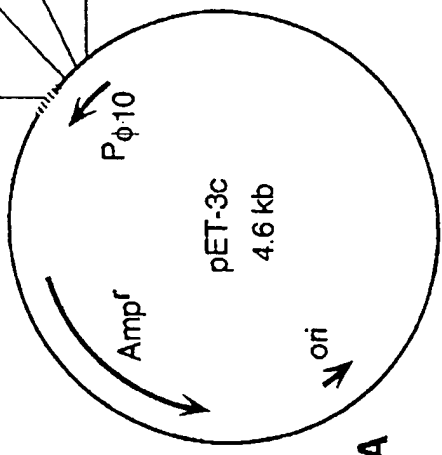
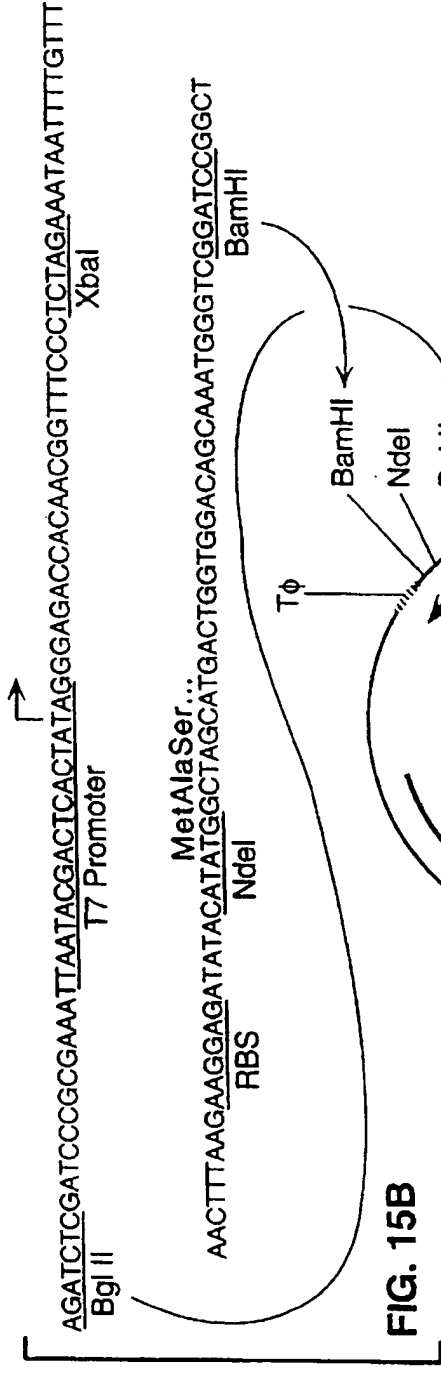
FIG. 13B



**FIG. 14B**



**FIG. 14C**



P<sub>φ10</sub>: Bacteriophage T7 φ10 promoter      RBS: Ribosome binding site

Tφ: T7 φ Terminator

**FIG. 15C**

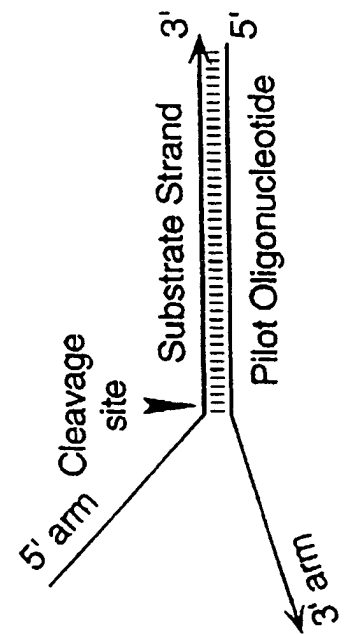


FIG. 16A

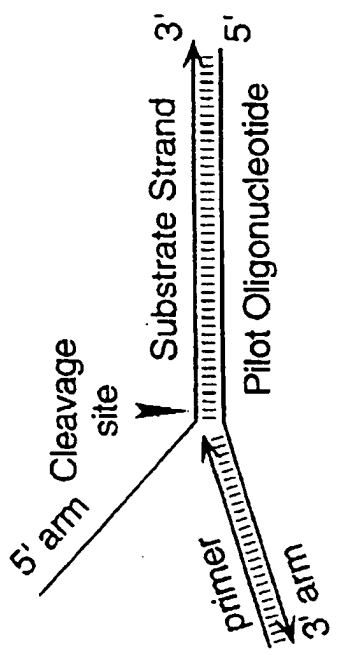


FIG. 16B

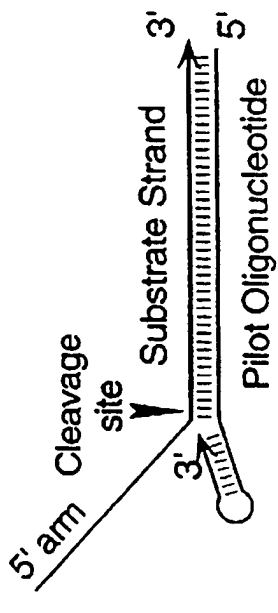


FIG. 16C

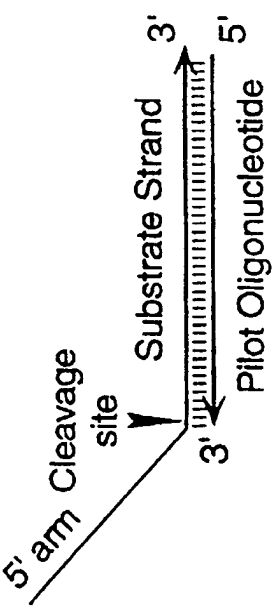


FIG. 16D

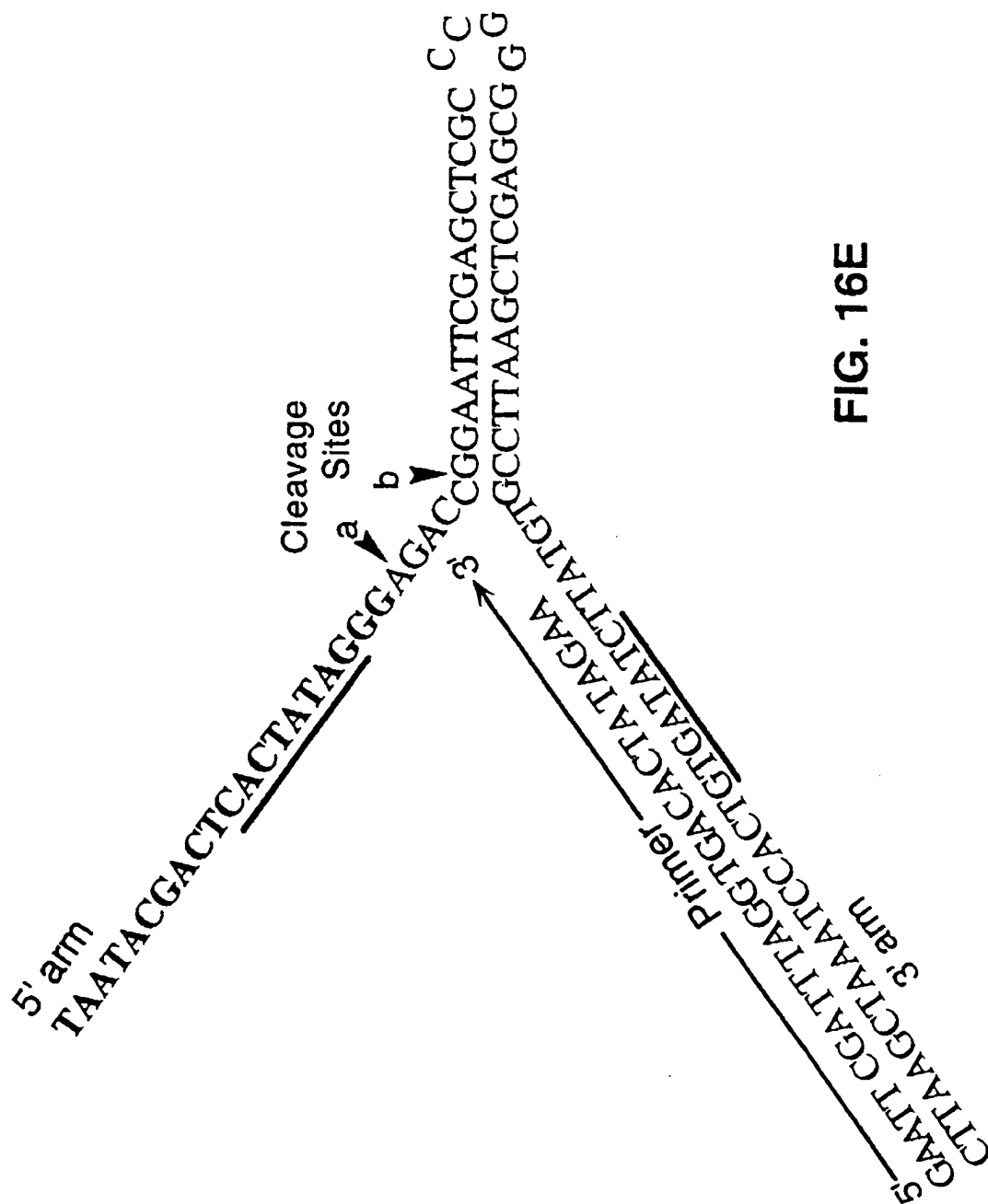


FIG. 16E

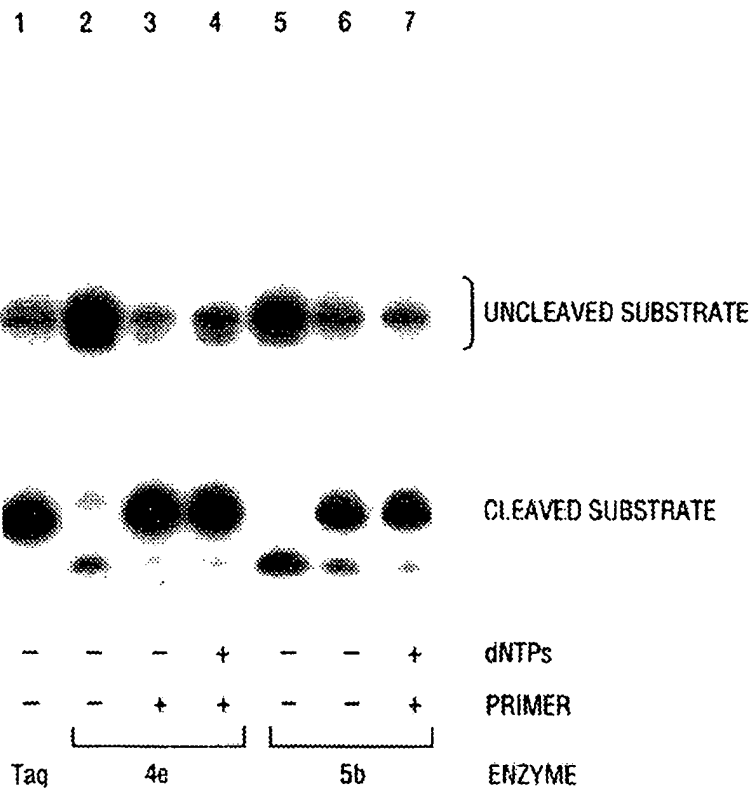


FIG. 17

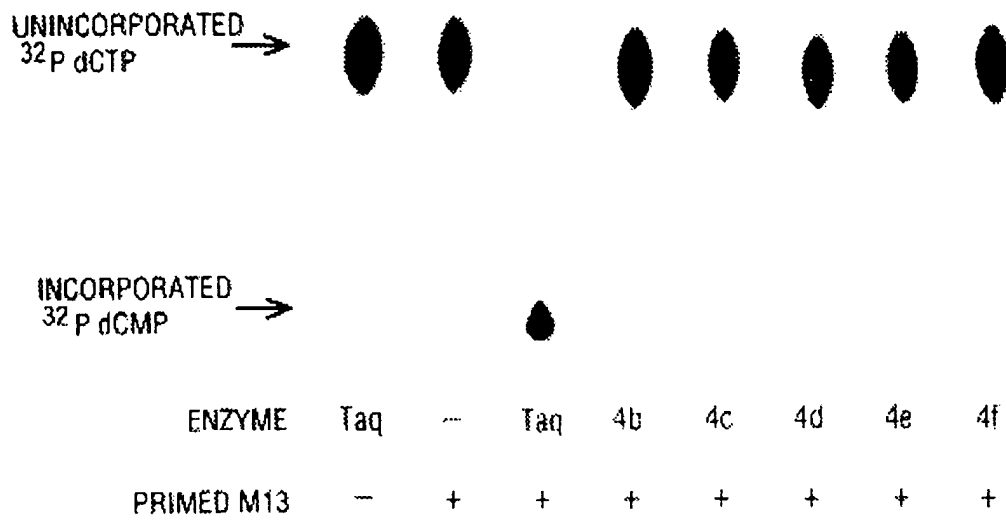


FIG. 18

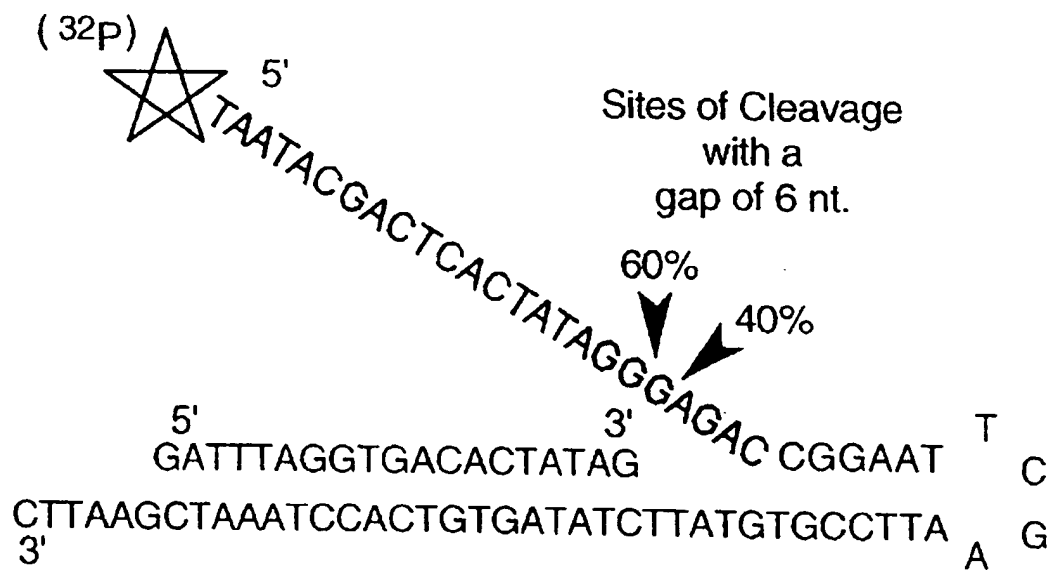


FIG. 19A

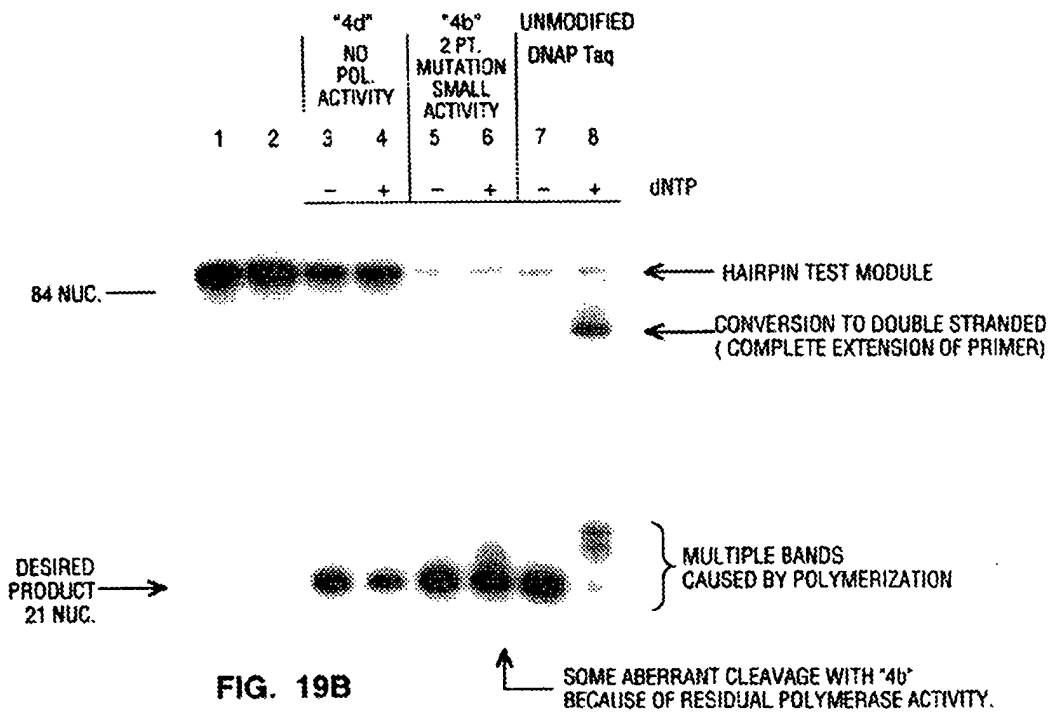
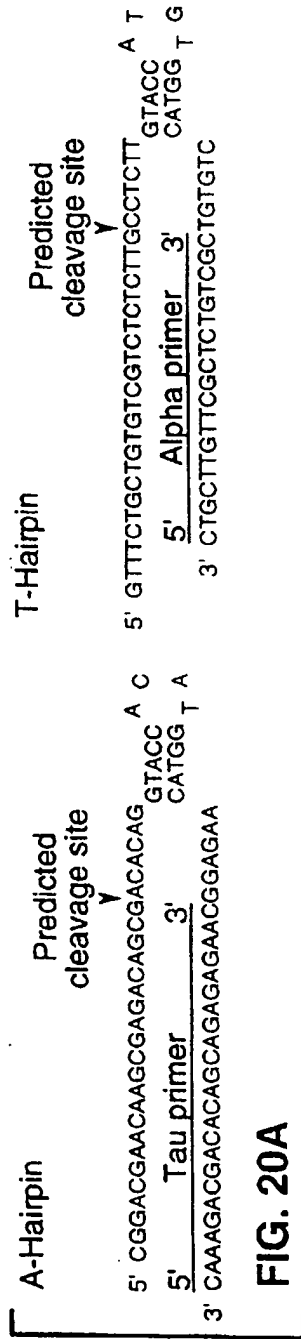


FIG. 19B



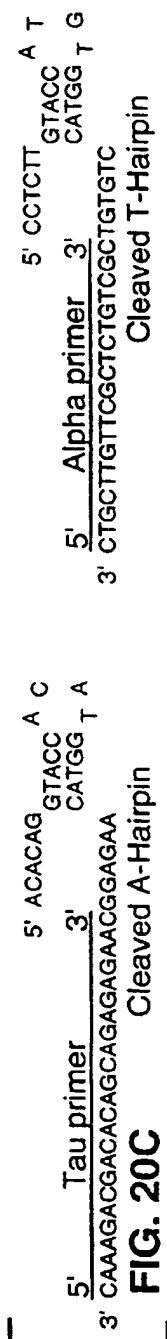


**FIG. 20A**

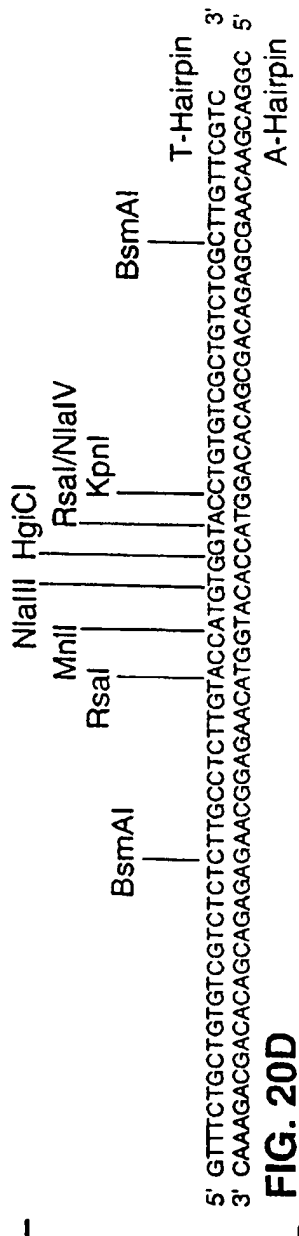
Sequence of alpha primer:

5' GACGAAACAAGCGAGACACGCG 3'

**FIG. 20B**



**FIG. 20C**



**FIG. 20D**

*Ban II*  
*Sst I*  
*Asp 718*  
*Ava I*  
*Kpn I*  
*Xma I*  
*Sma I*  
*EcoR I*  
*Bam HI XI*

CCCCAGGGTTTCCCGAGTCACGACGTTGTAAACGACGGCCAGTGAATTGTAAATACGACTCACTATAGGCCGAAATTCGAGGTCGGTACCCGGGATCCTC  
 GCGGTCCCAAAGGGTCAGTGCCTGCAACAATTTGCTGCCGGTCACCTTAACAATTAATGCTGAGTGATATCCCGCTTAAGCTCGAGCCATGGGCCCCCTAGGAG

——— -47 Forward ———  
 ——— 17 ———  
 ——— Pilot 30-0 ———

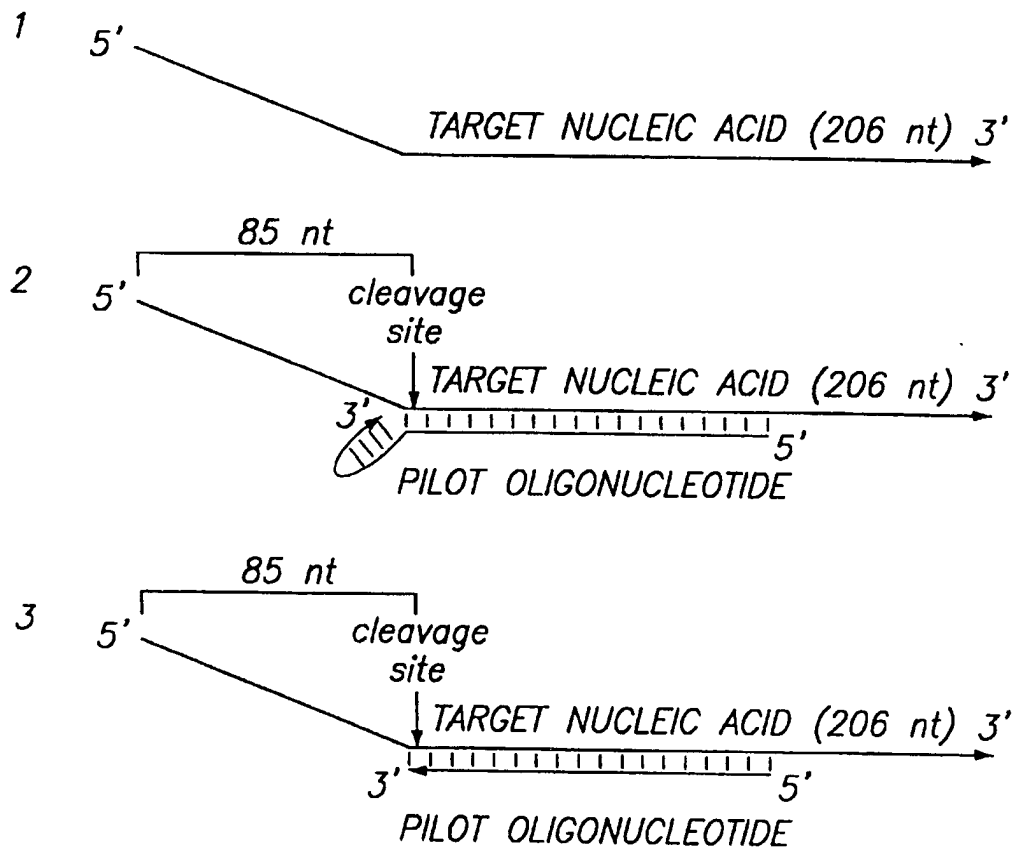
*Sal I*  
*Pst I*  
*BspM I*  
*Acc I*  
*Hinc II*  
*Sph I*  
*Hind III*

TAGAGTCGACCTGCAGGCAATGCAAGCTTGAGTATTCATAGTGCACCTAAATAGCTTGGCGTAAATCATGGTCAATAGCTGTTTCCCTGCTGTAATTTGTTA  
 ATCTCAGCTGGACGTCGGTAGCTTGAACATCAAGATATCACAGTGGATTTATCGAACCCGCAATAGTACCAGTATCGACAAAGGACACACACTTTAAACAAT

——— Pilot 30-0 ———  
 ——— SP6 ———  
 ——— 2 ———  
 ——— -48 Reverse ———

TCCGCTCACAAATCCACACACAACATACGA 228  
 AGCGAGTGTAAAGGTGTGTGTATGCT  
 ——— -48 Reverse ———  
 ——— 206 ———

FIG. 21

**FIG. 22A**

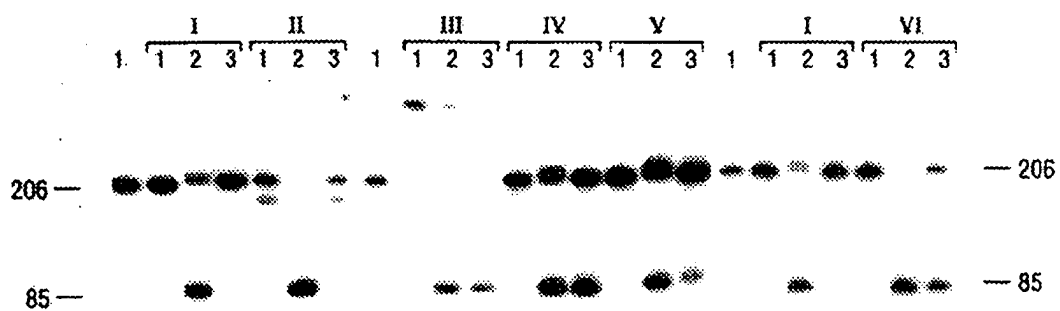


FIG. 22B

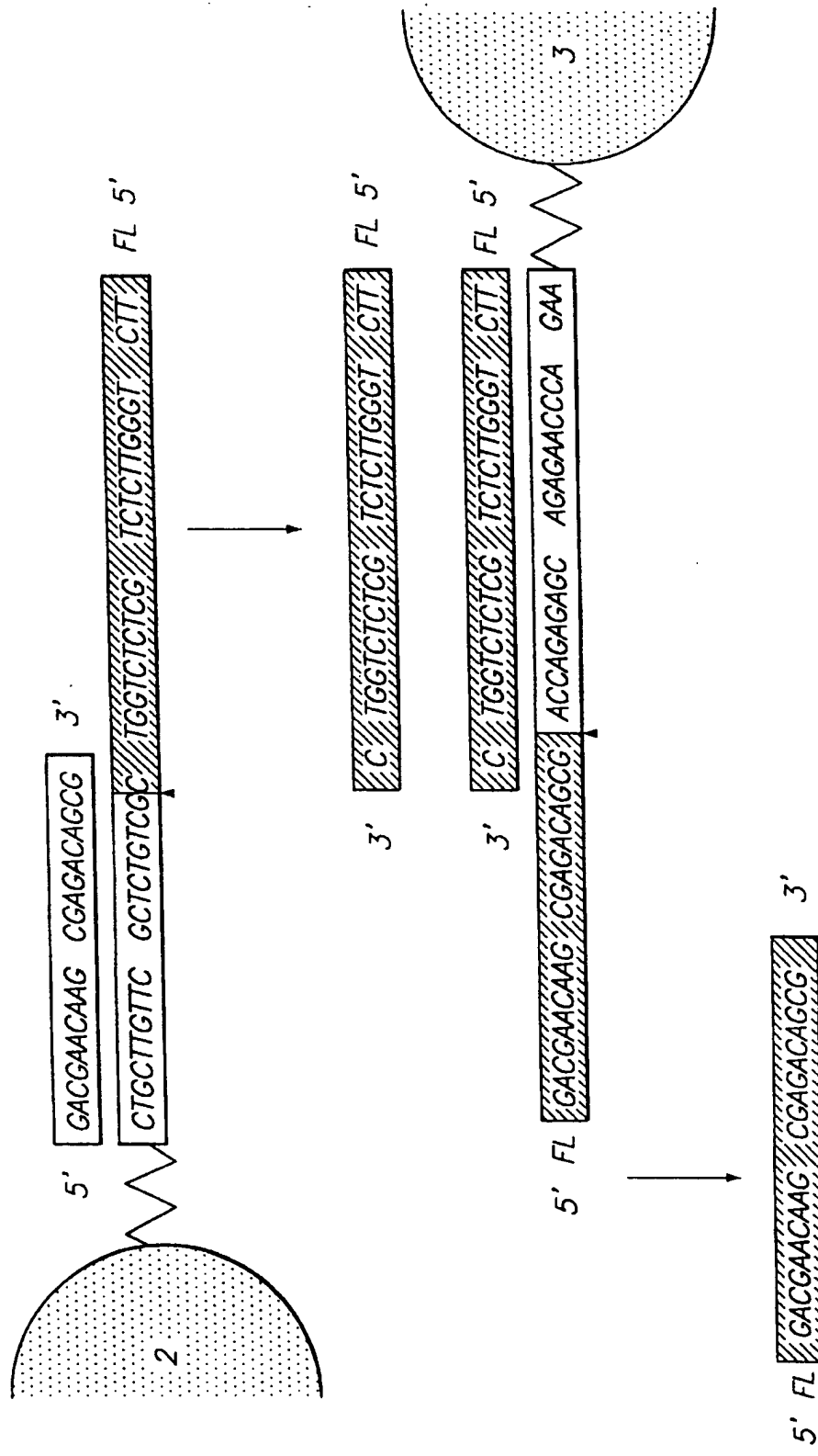


FIG. 23

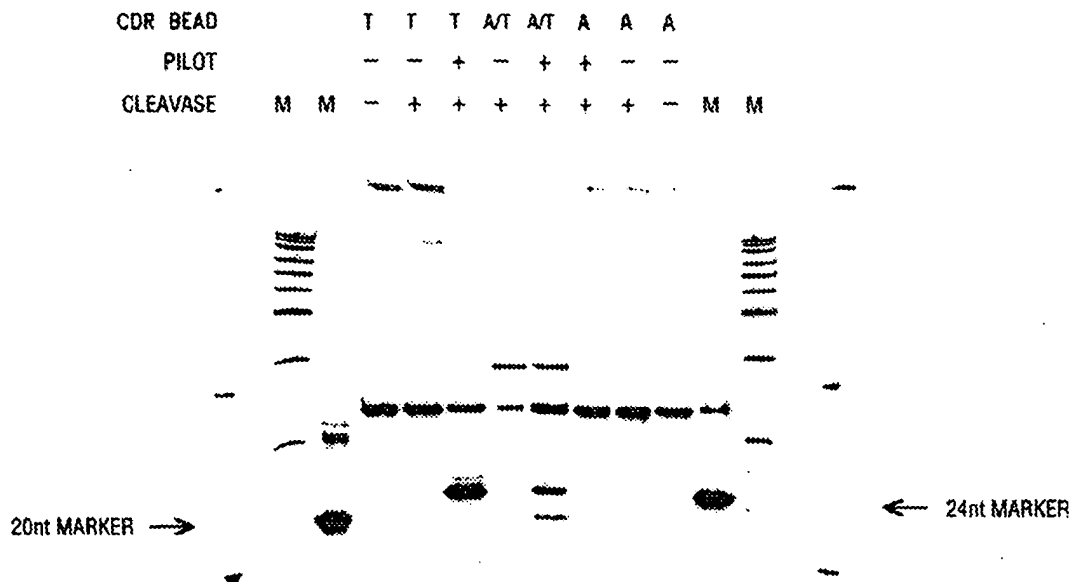


FIG. 24

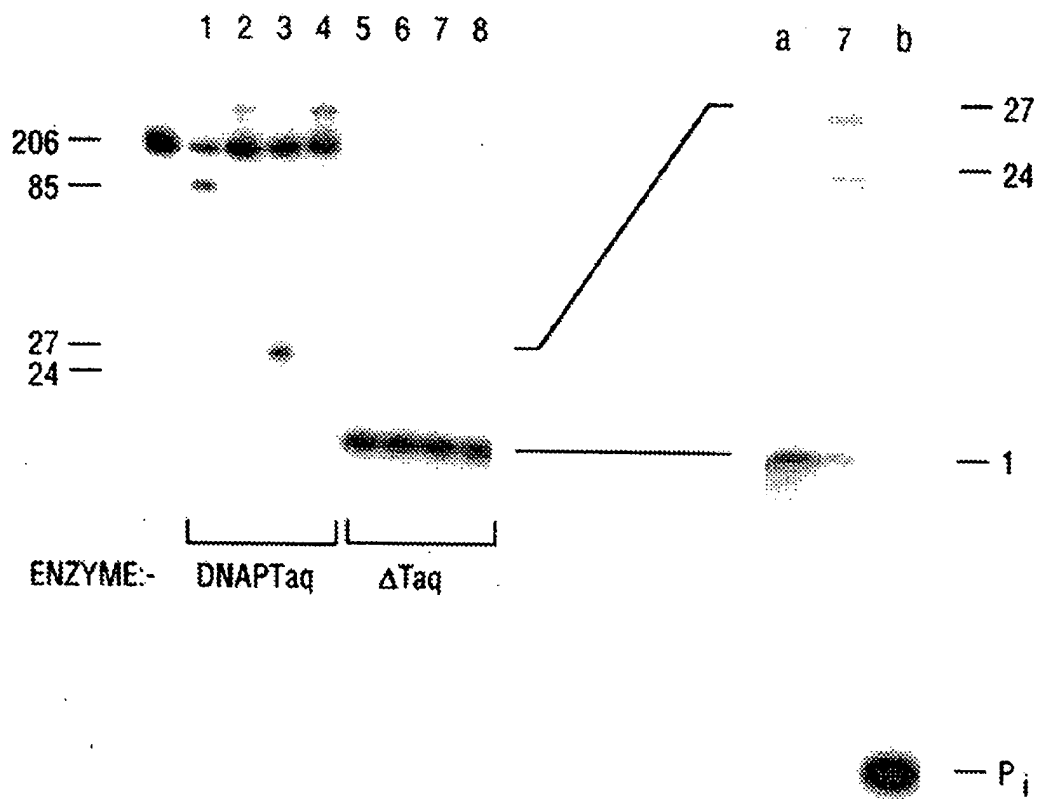


FIG. 25A

FIG. 25B

FIG. 26A

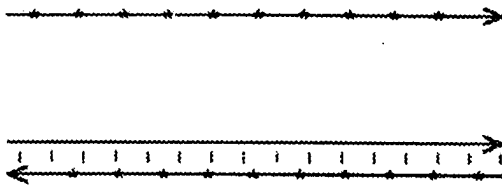
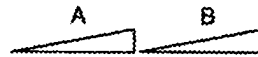


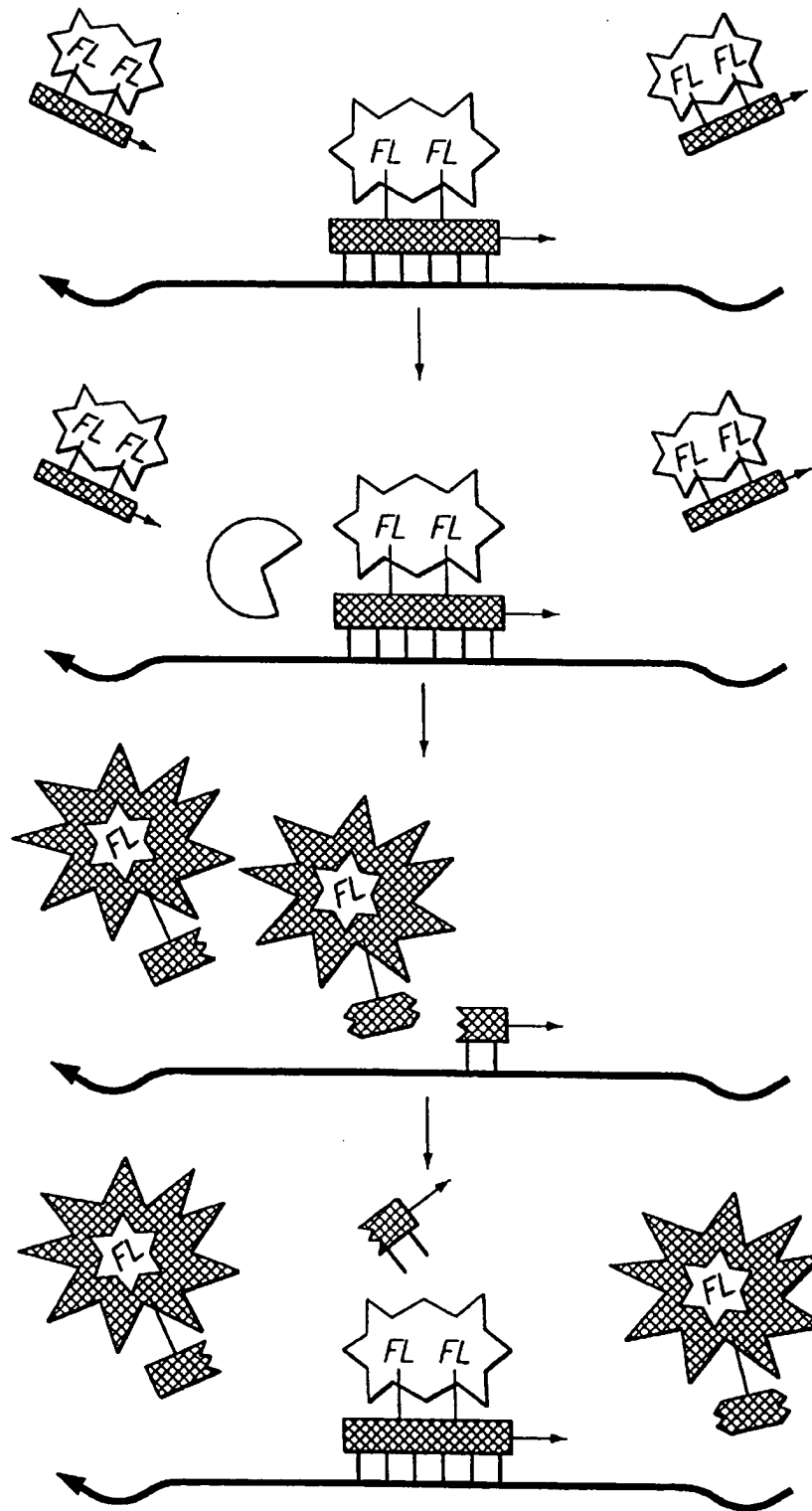
FIG. 26B

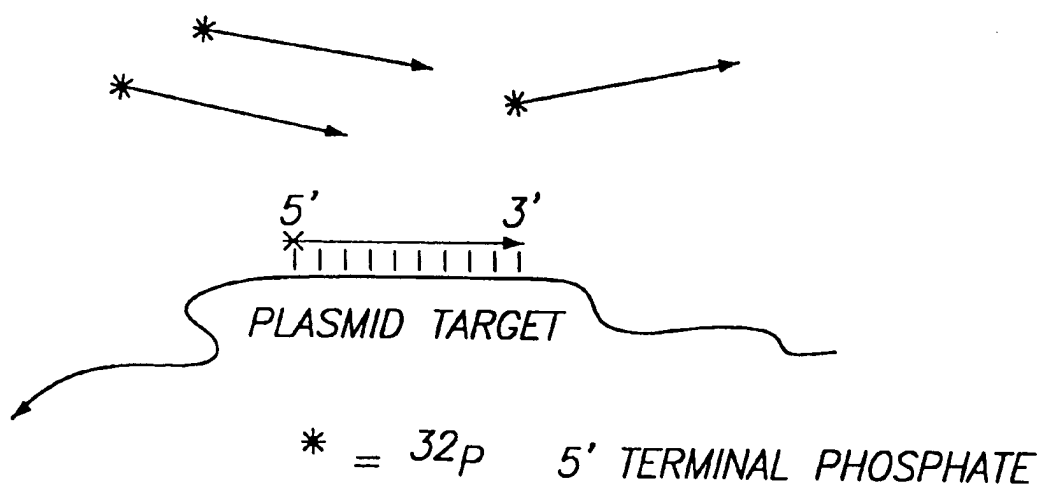
\* = 32p

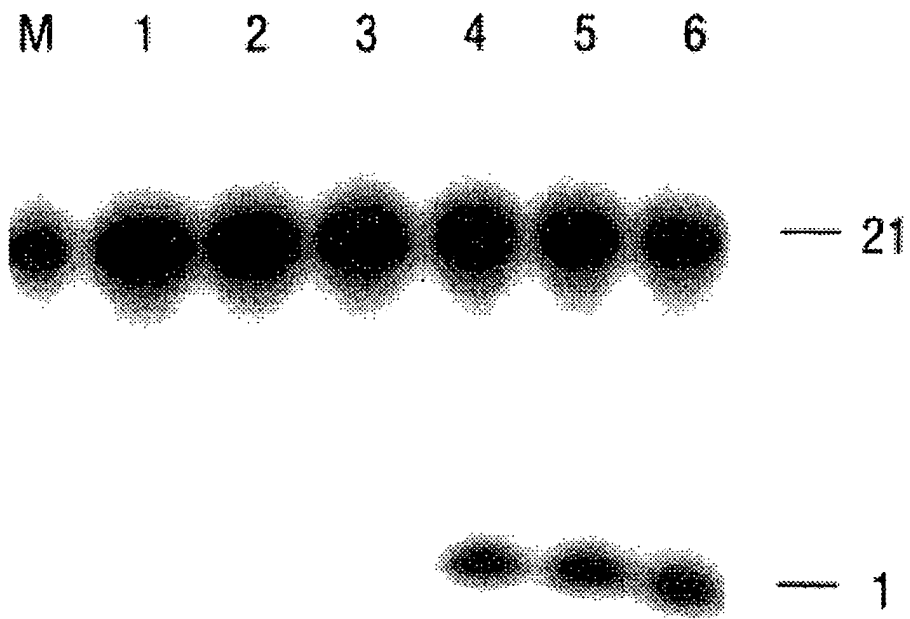


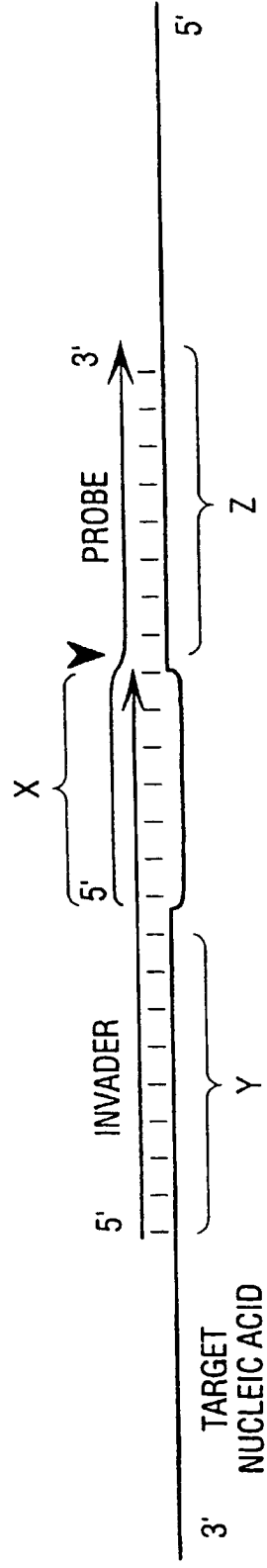
— 206



**FIG. 27**

**FIG. 28A**

**FIG. 28B**



**FIG. 29**

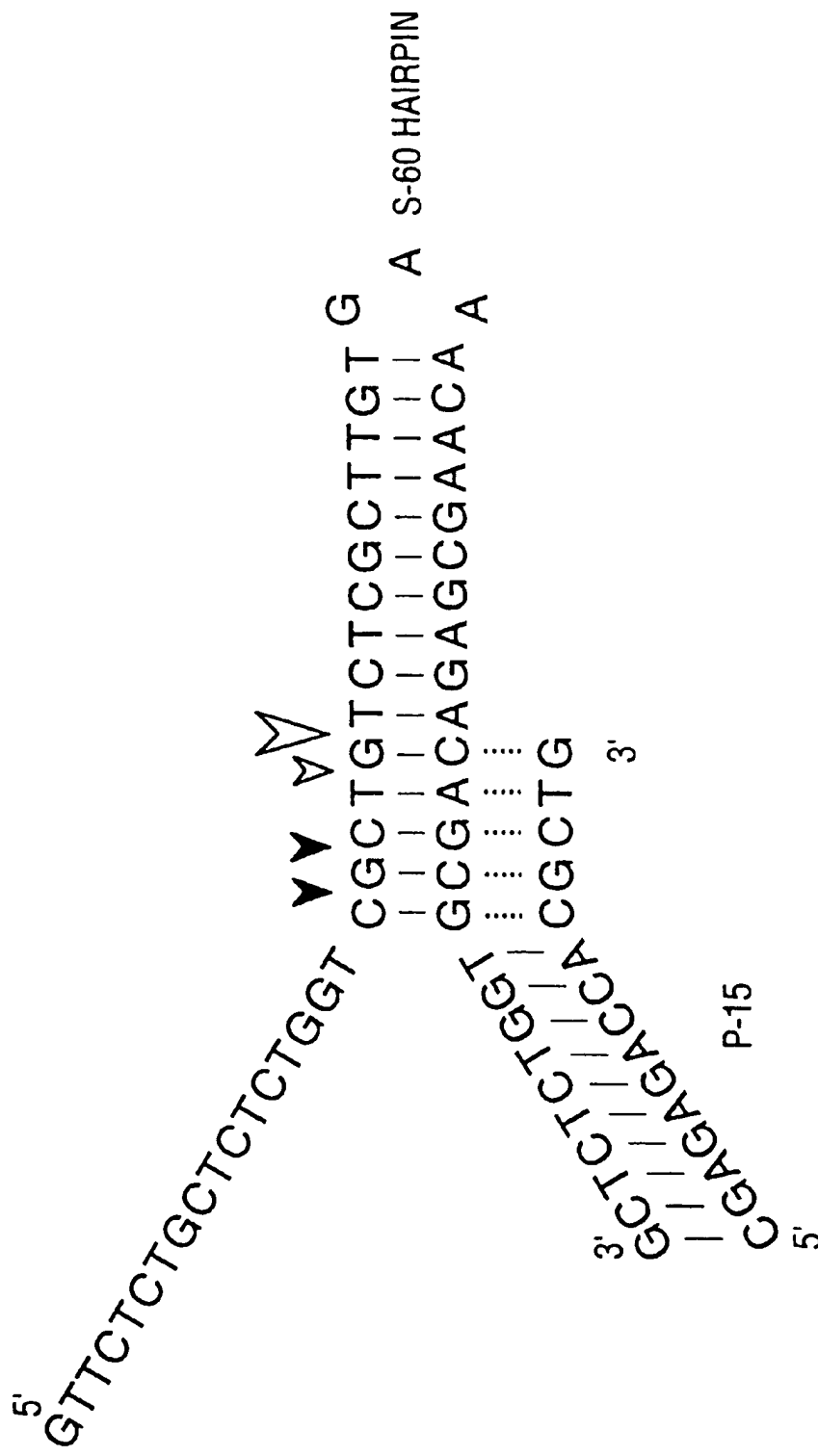
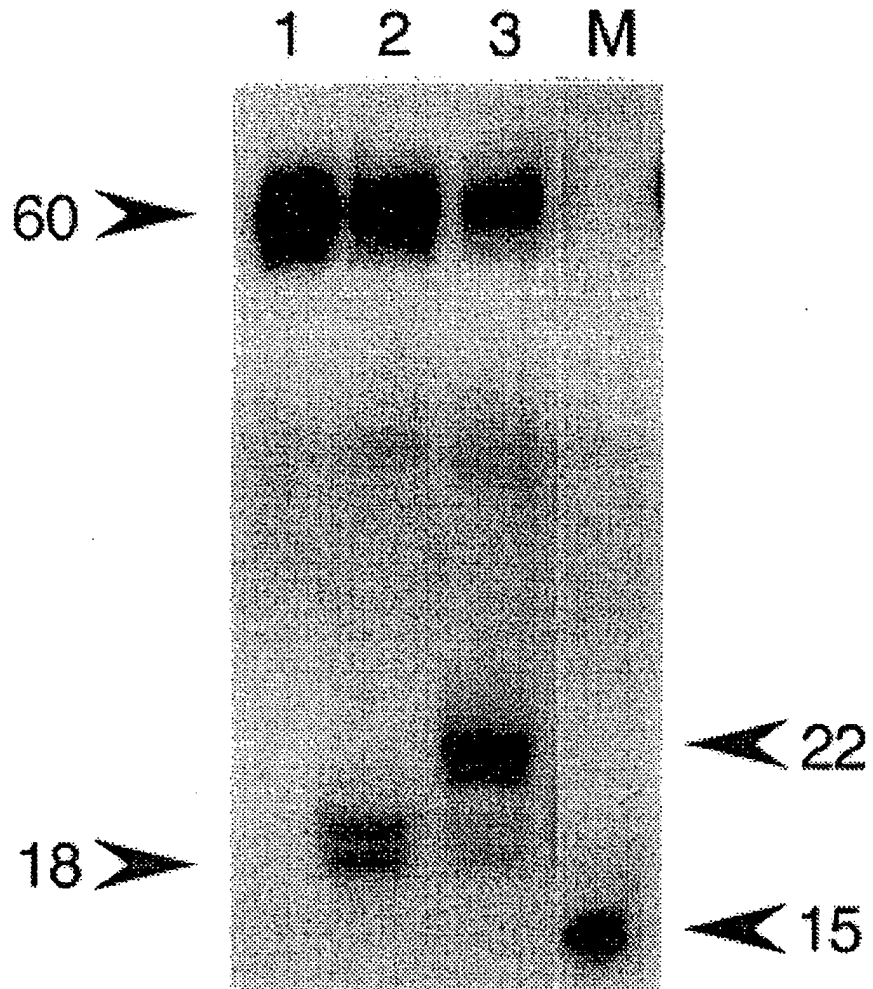


FIG. 30



**FIG. 31**

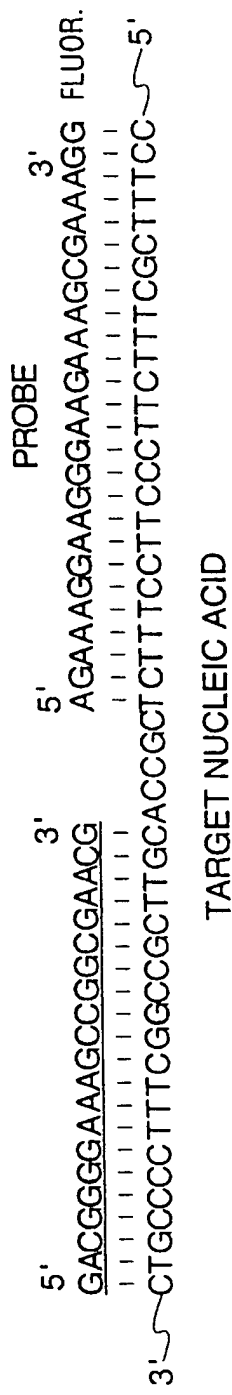


FIG. 32A

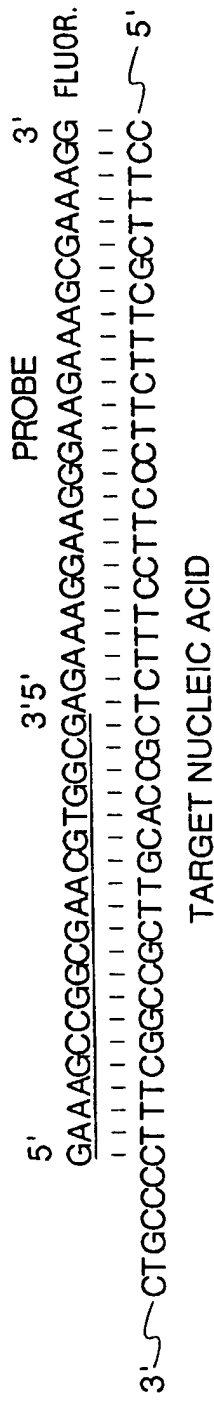


FIG. 32B

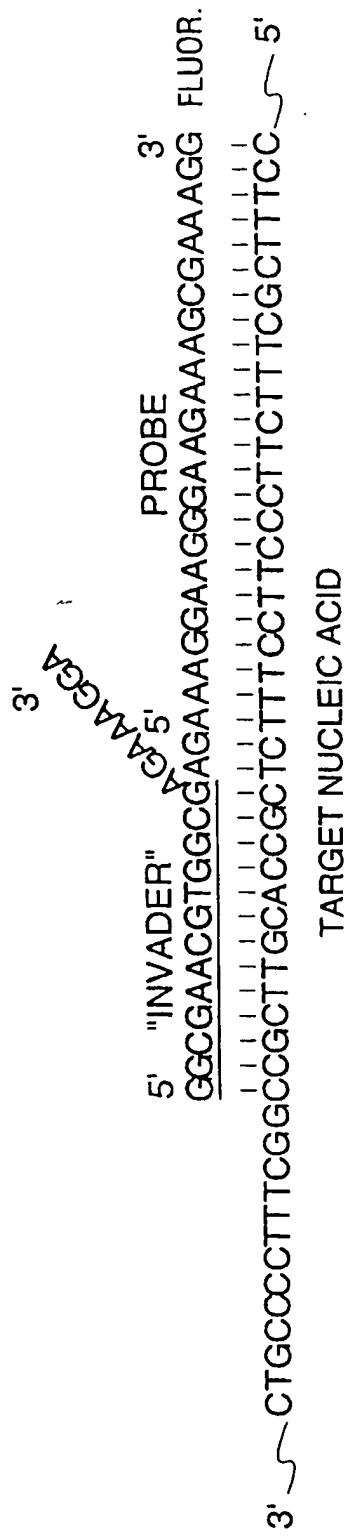


FIG. 32C

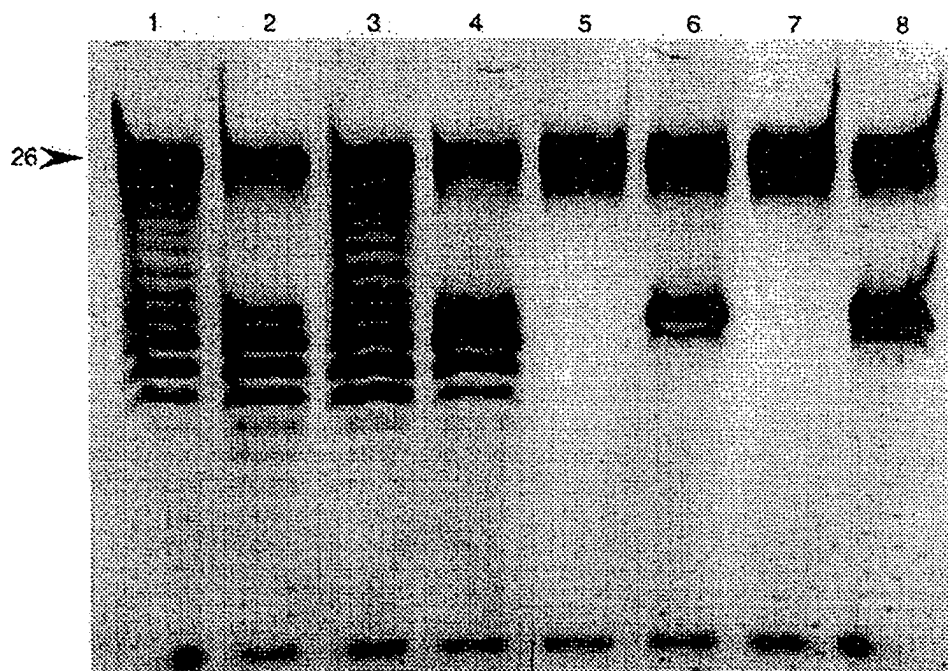


FIG. 33



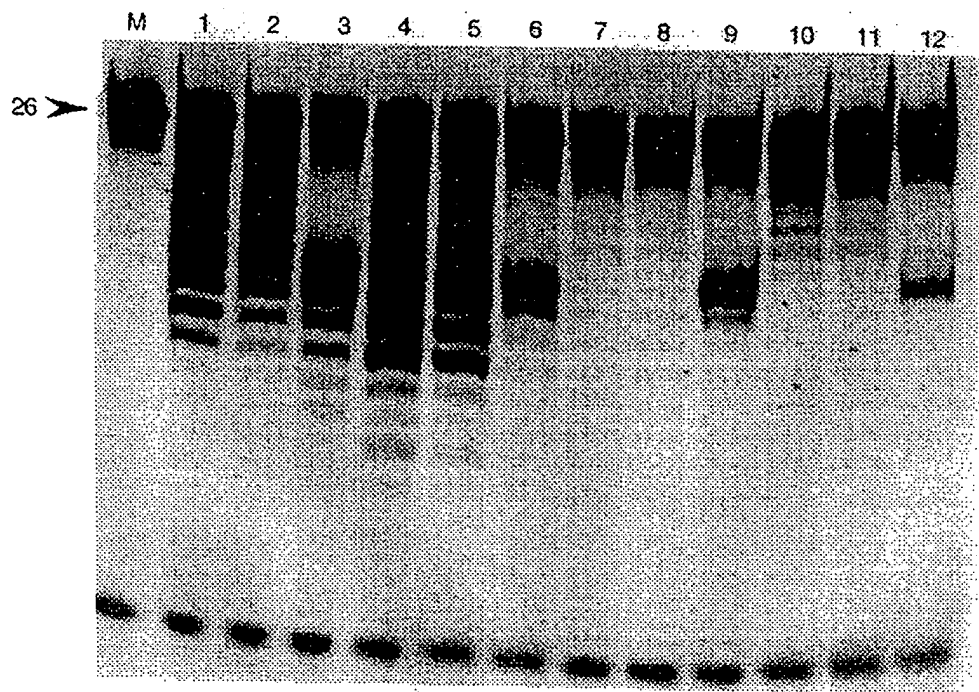


FIG. 34

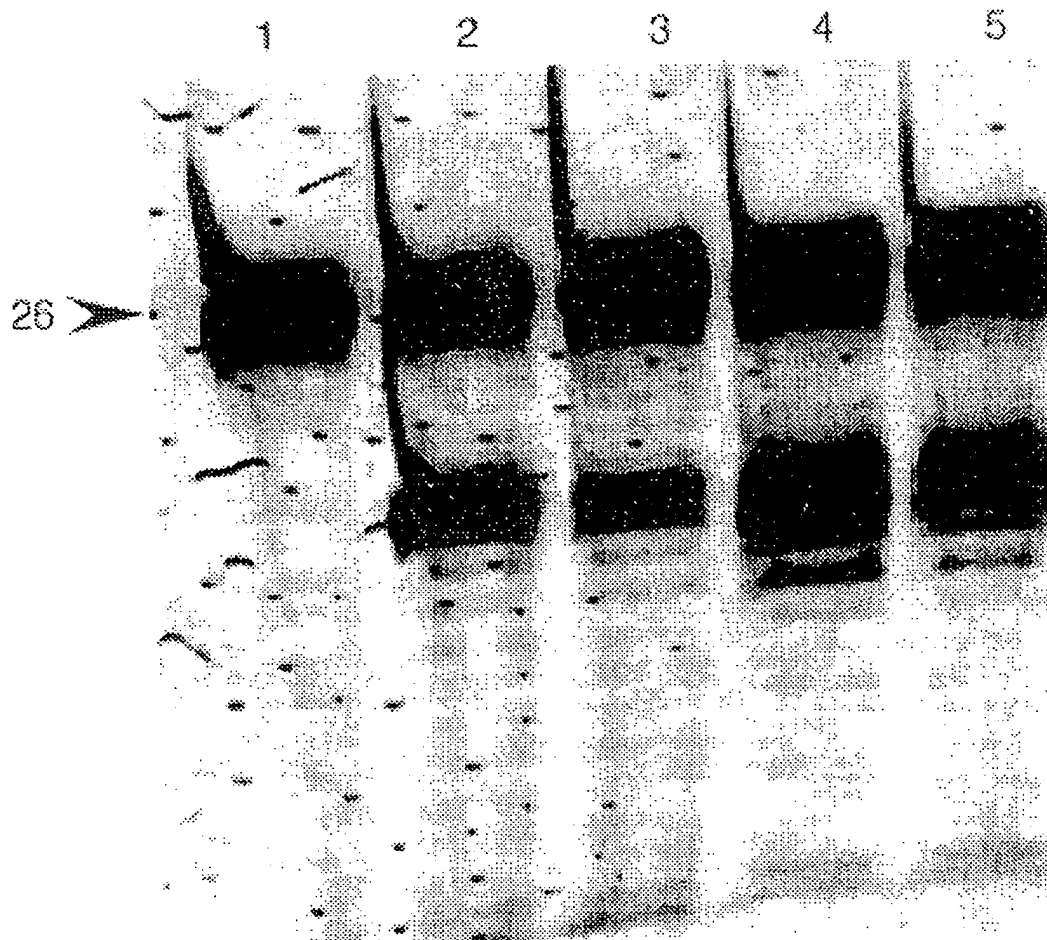


FIG. 35

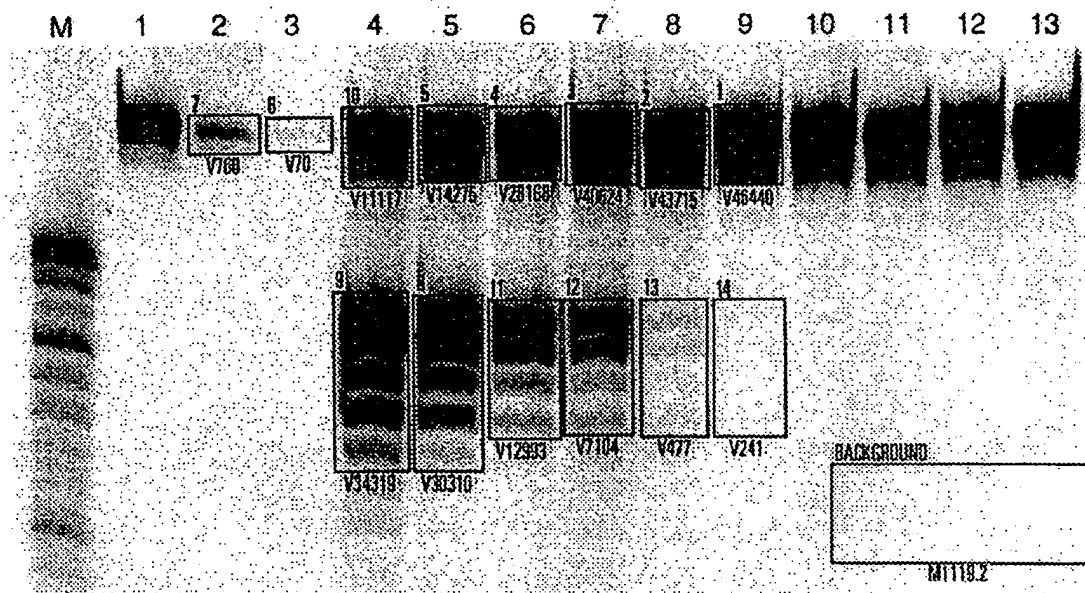
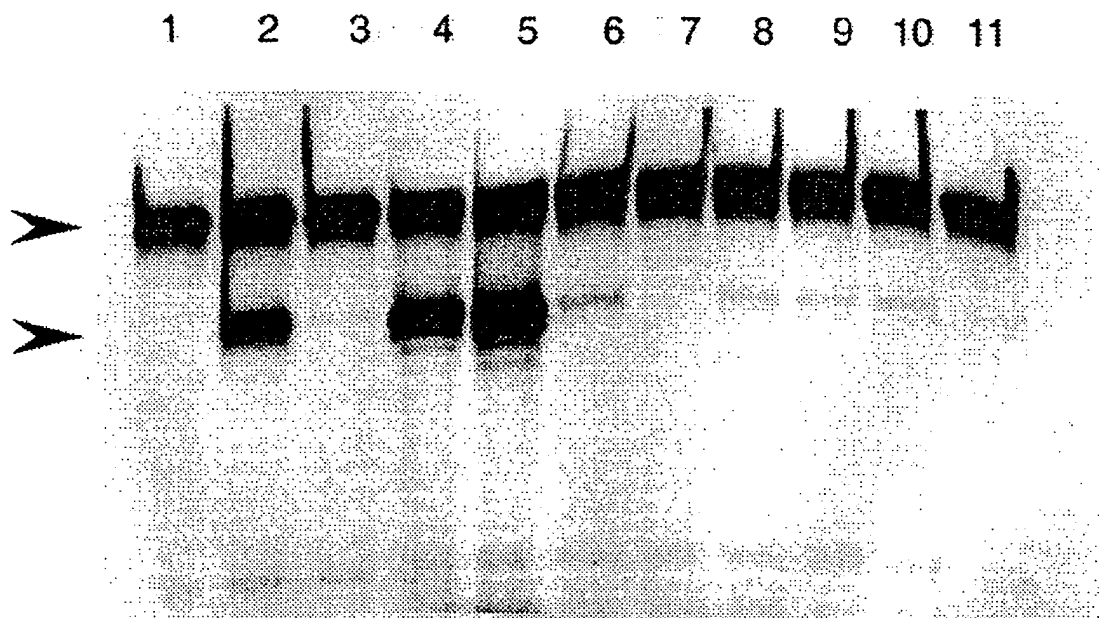
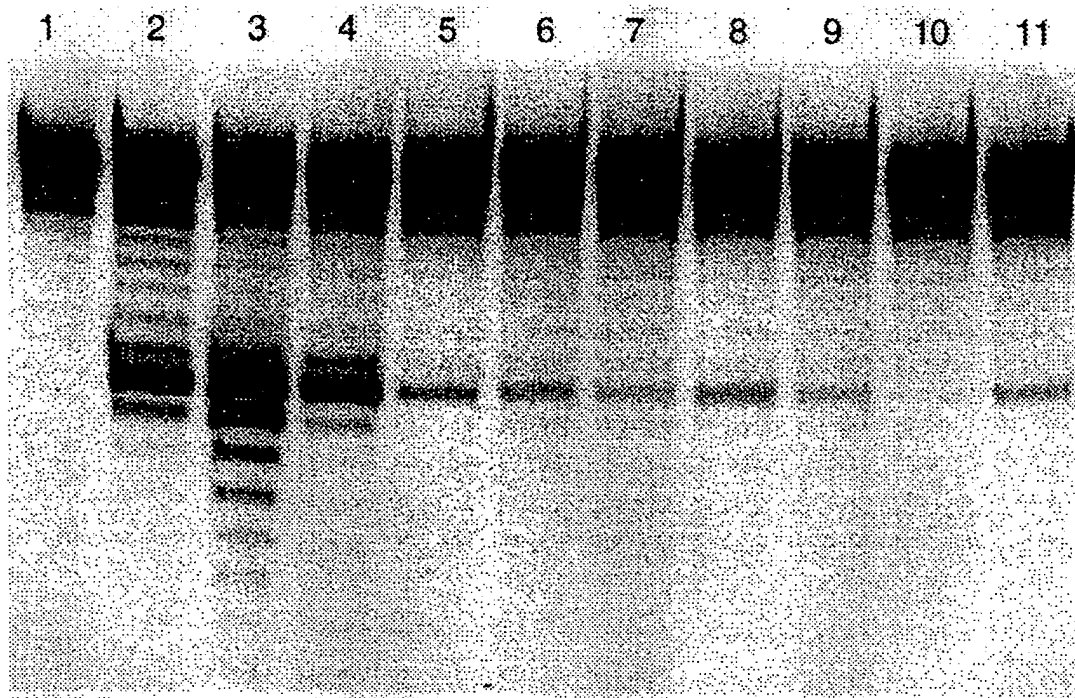
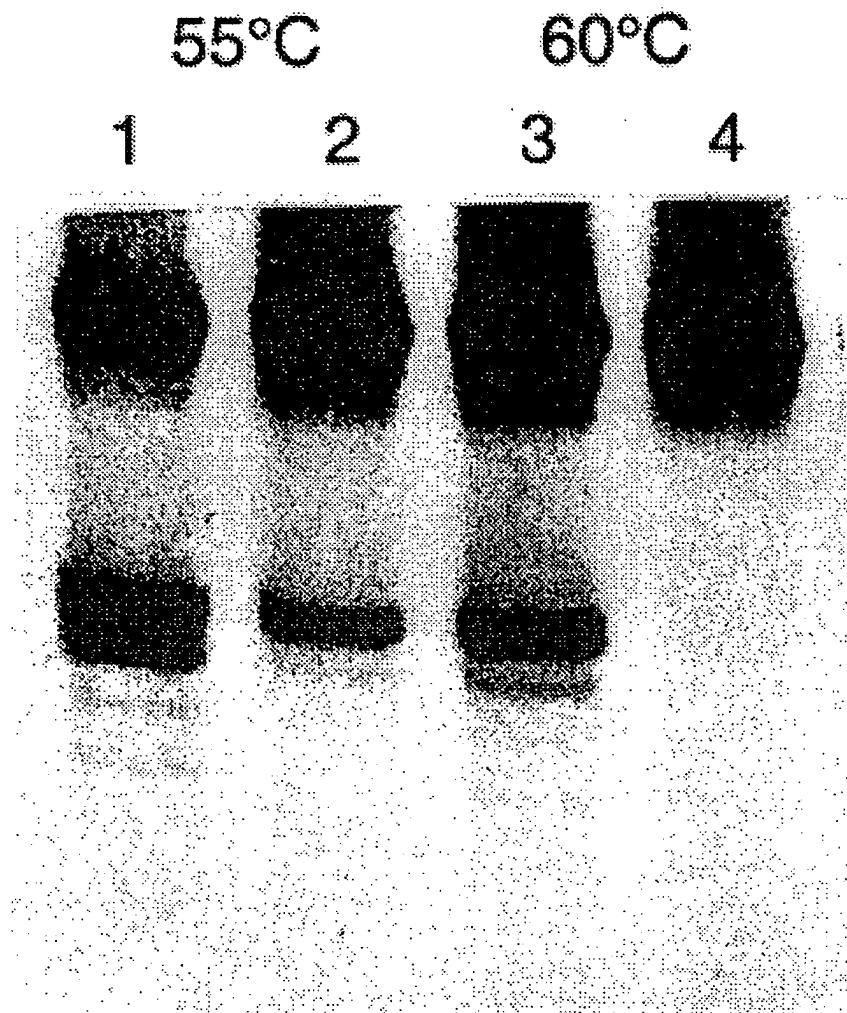


FIG. 36

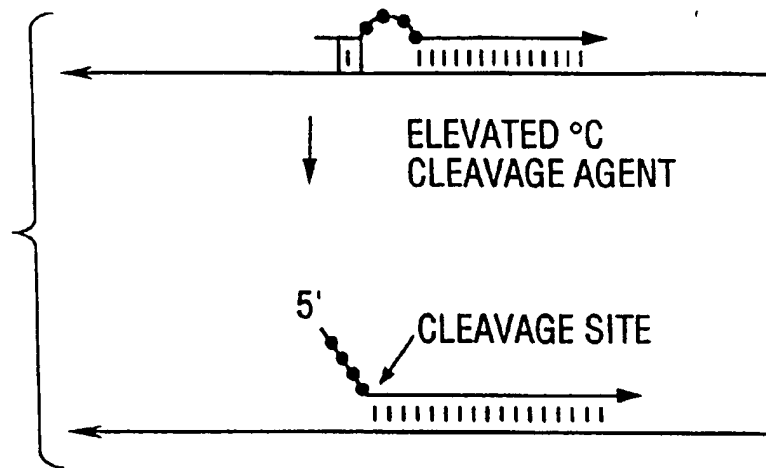
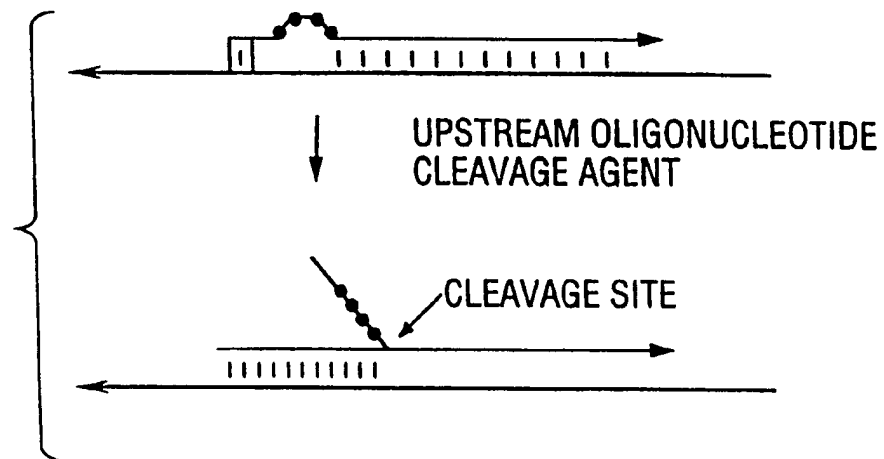


**FIG. 37**

**FIG. 38**



**FIG. 39**

**FIG. 40A****FIG. 40B**

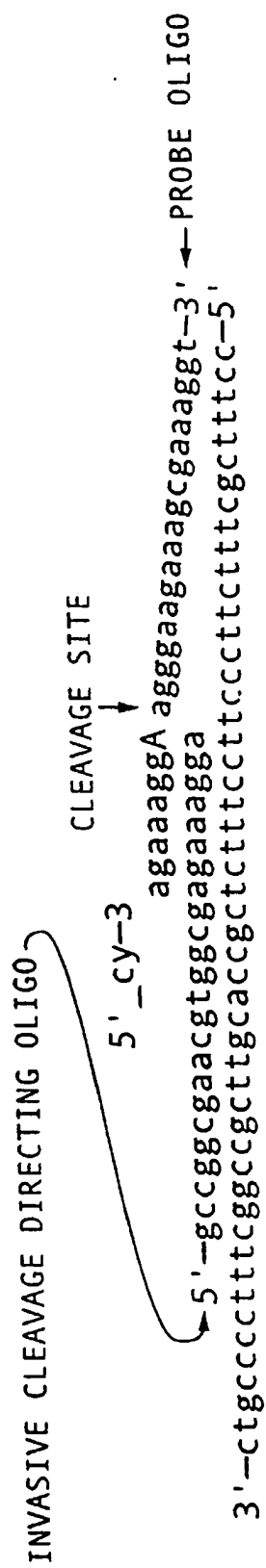
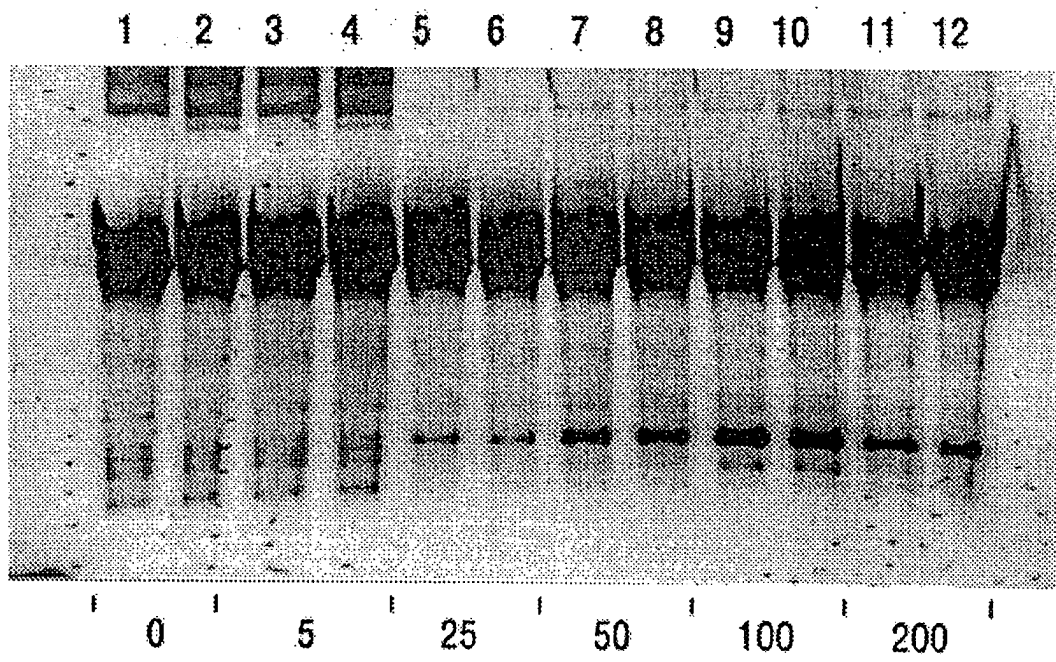
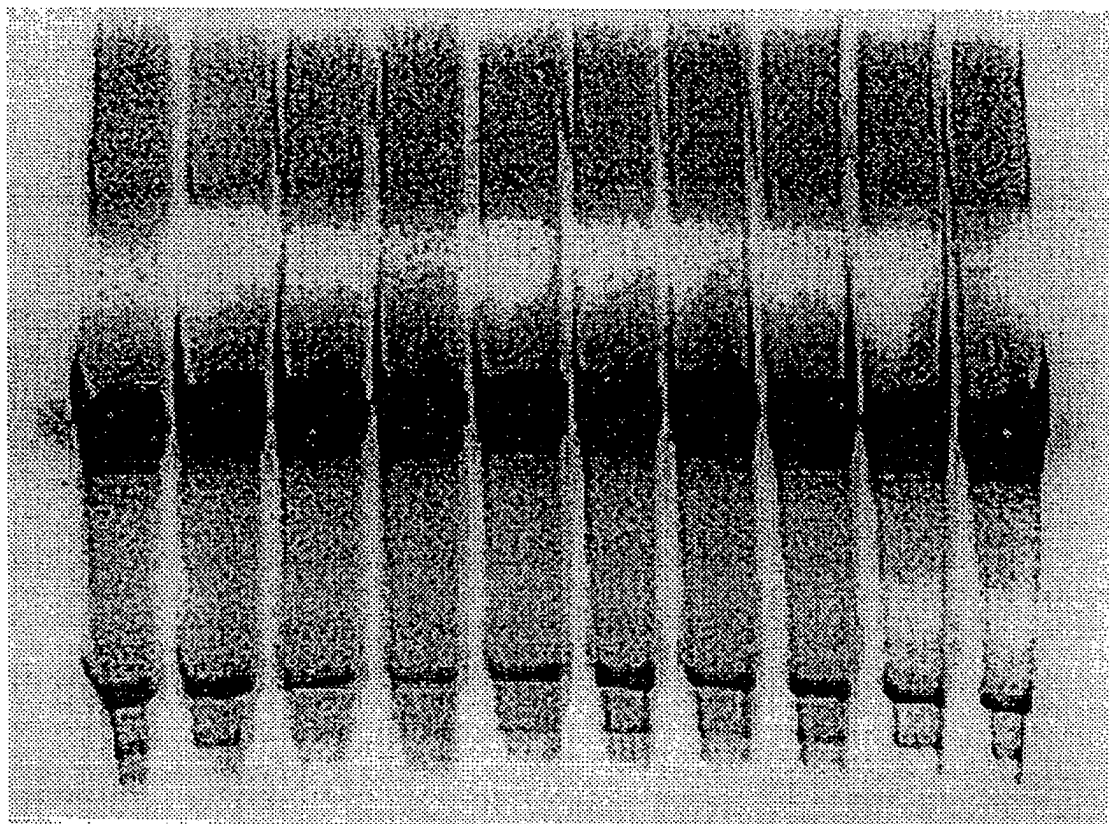


FIG. 41



**FIG. 42**

1 2 3 4 5 6 7 8 9 10



**FIG. 43**

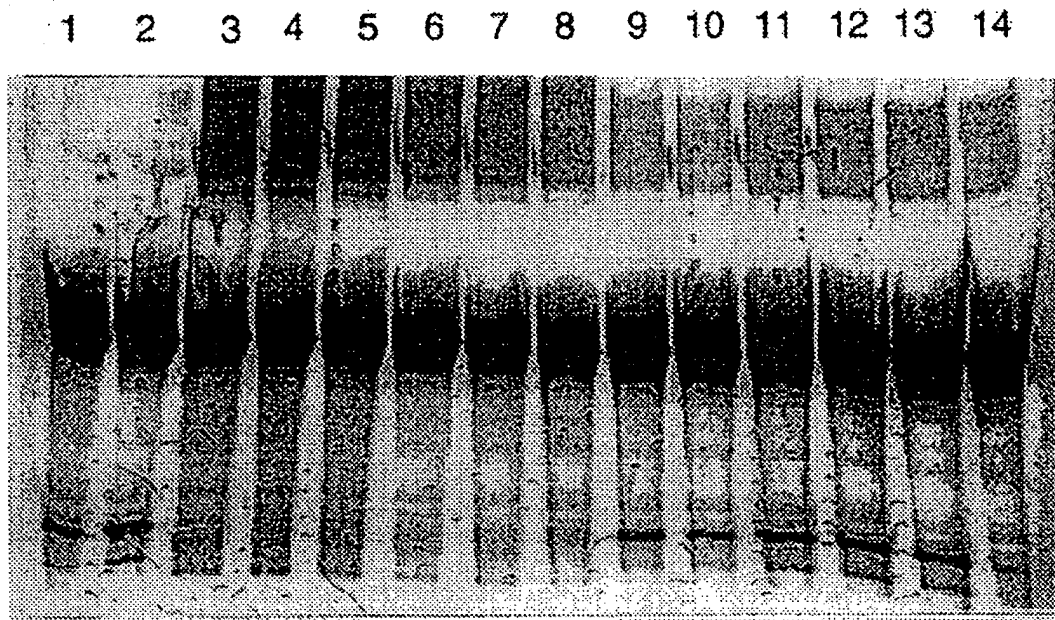


FIG. 44

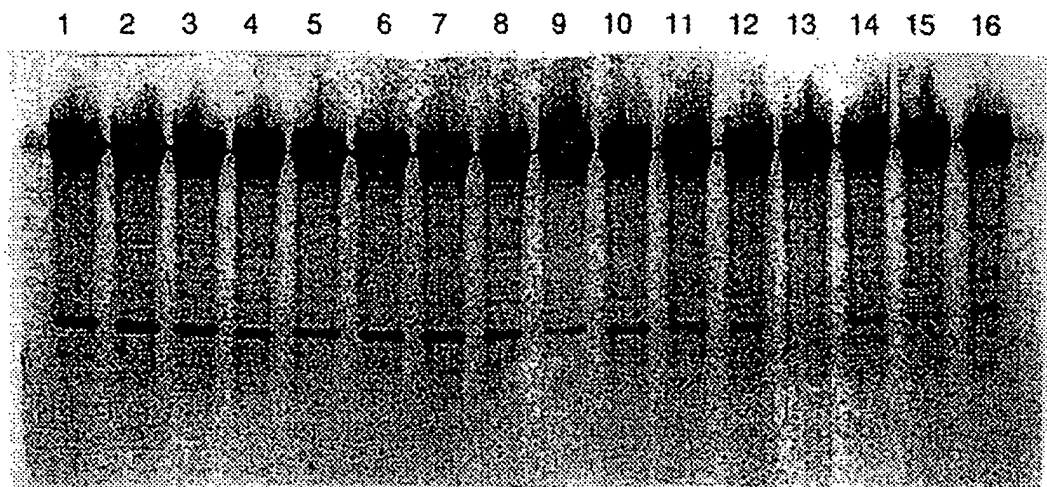


FIG. 45

1 2 3 4 5 6 7 8 9 10 11 12 13 14

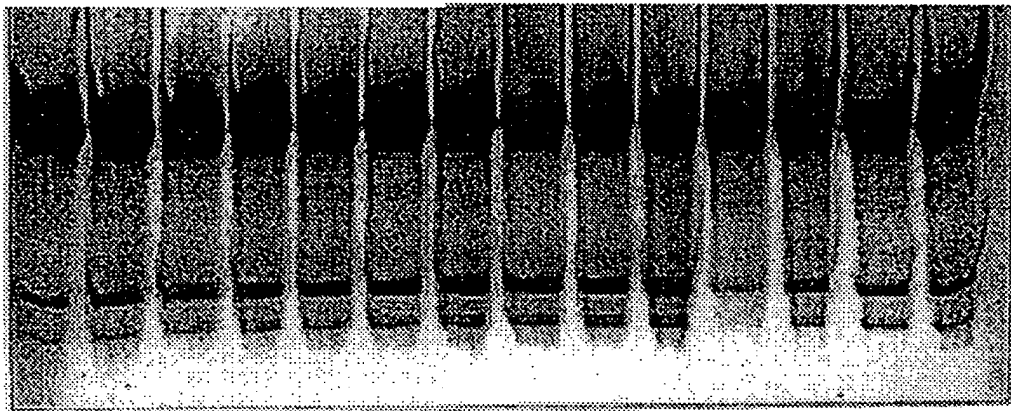


FIG. 46

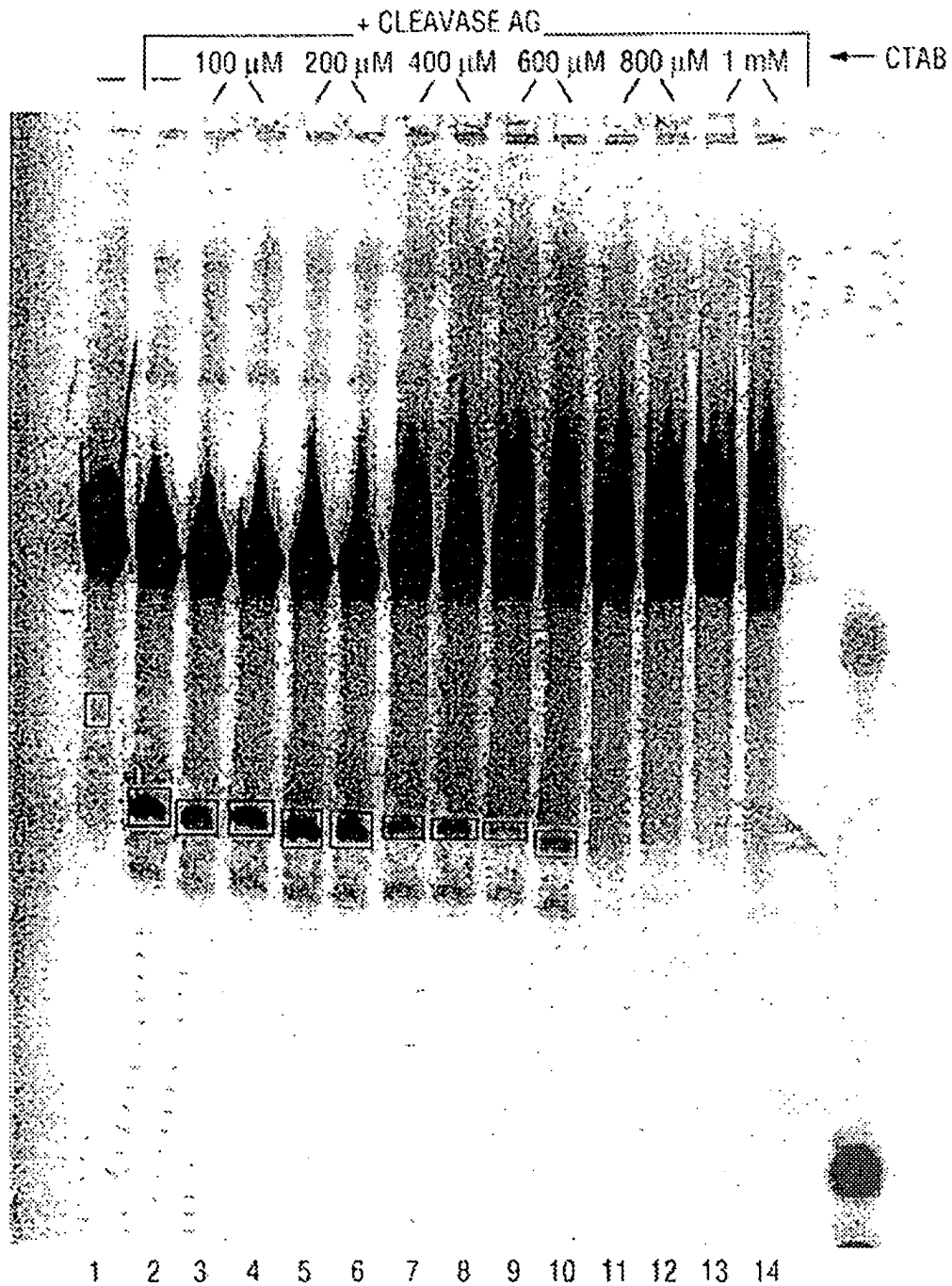
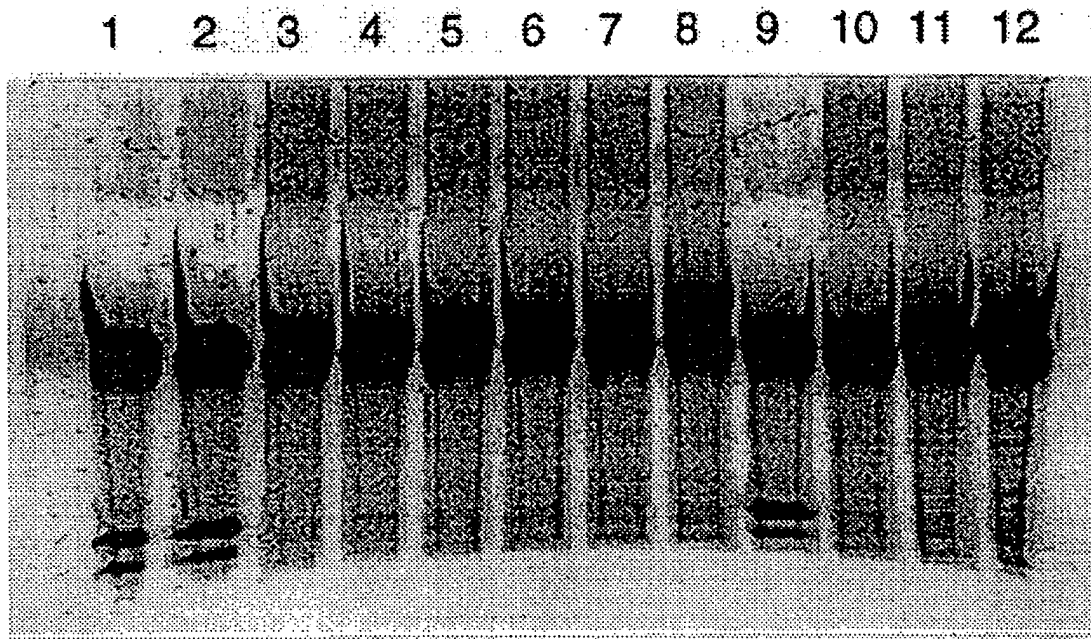
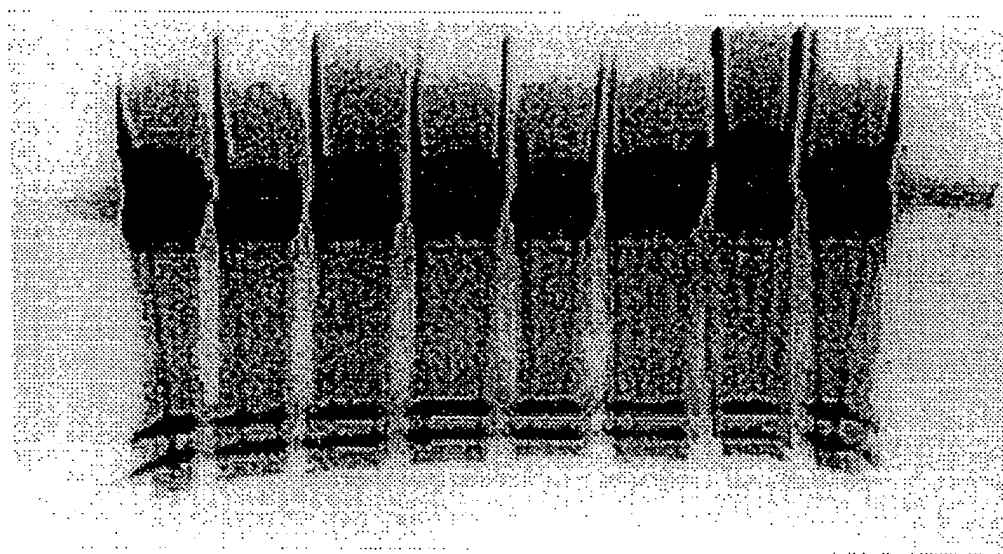


FIG. 47



**FIG. 48**

1 2 3 4 5 6 7 8



**FIG. 49**



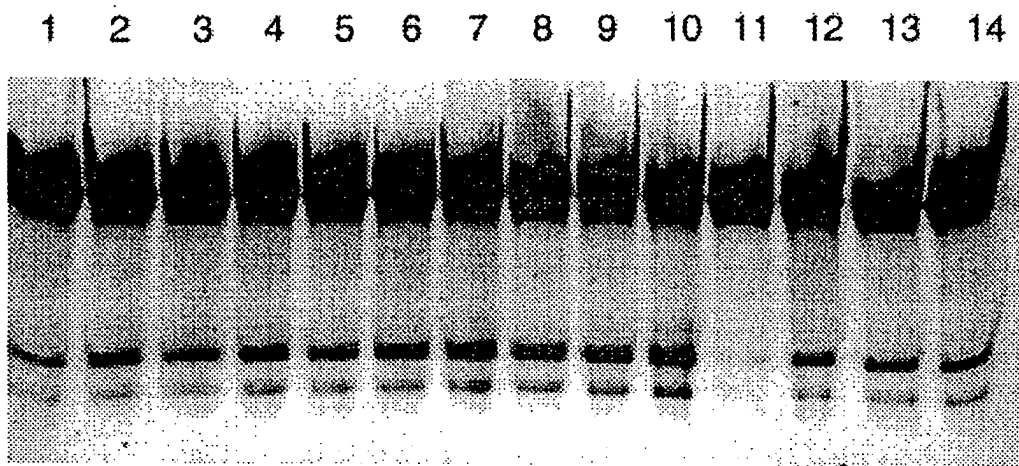
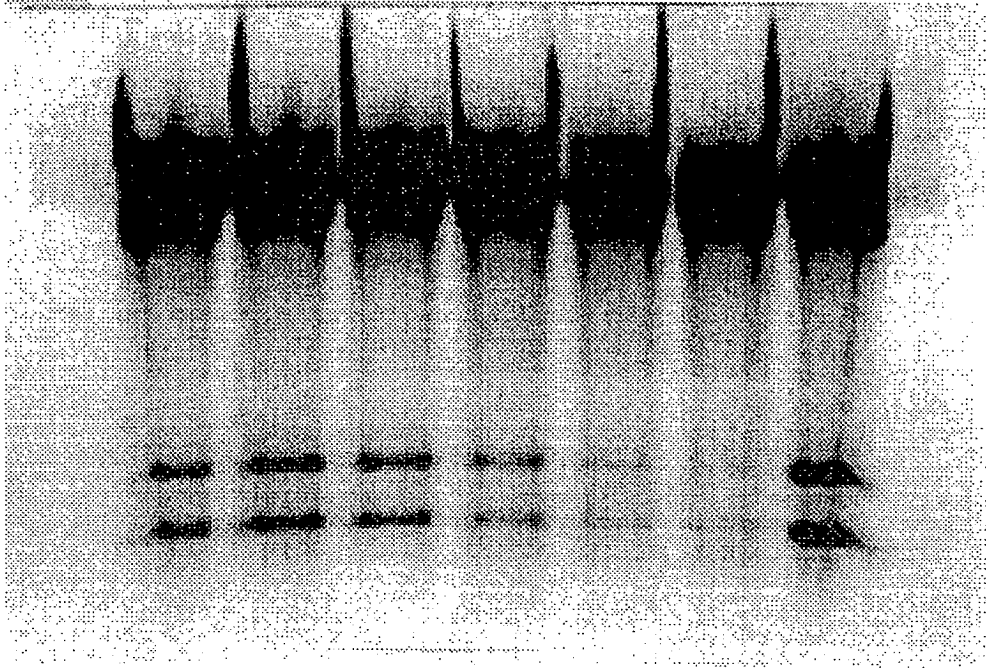
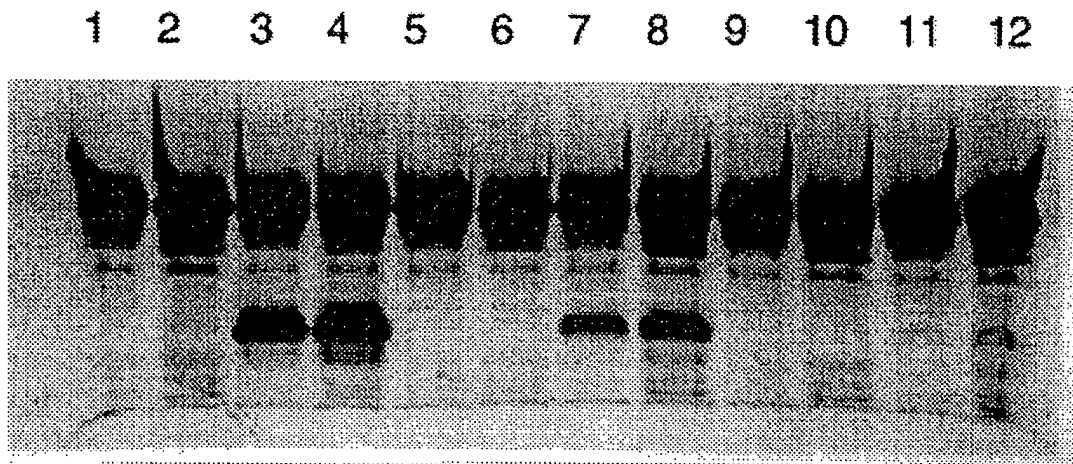


FIG. 50

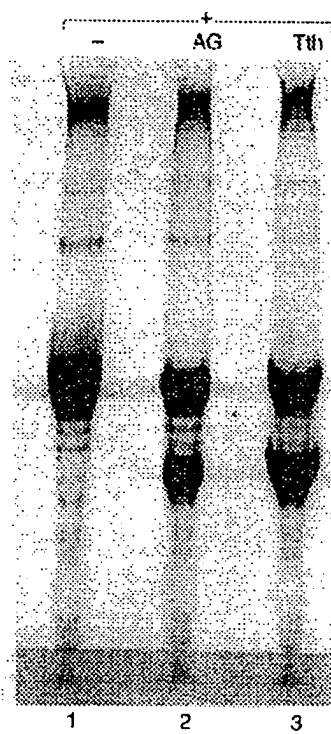
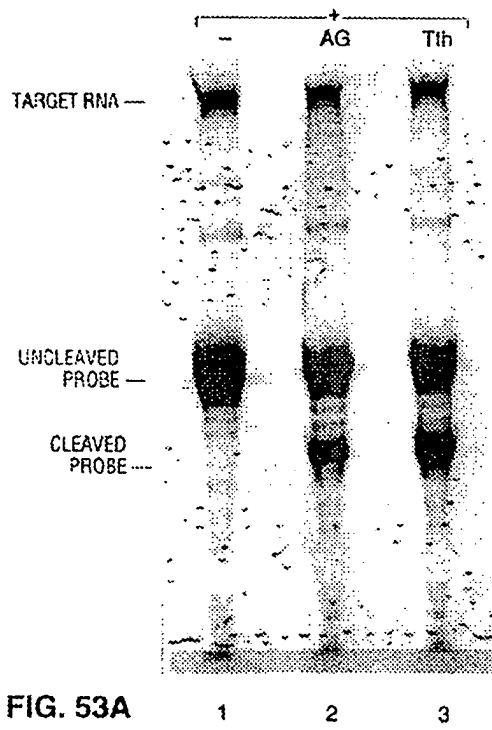
1 2 3 4 5 6 7



**FIG. 51**



**FIG. 52**



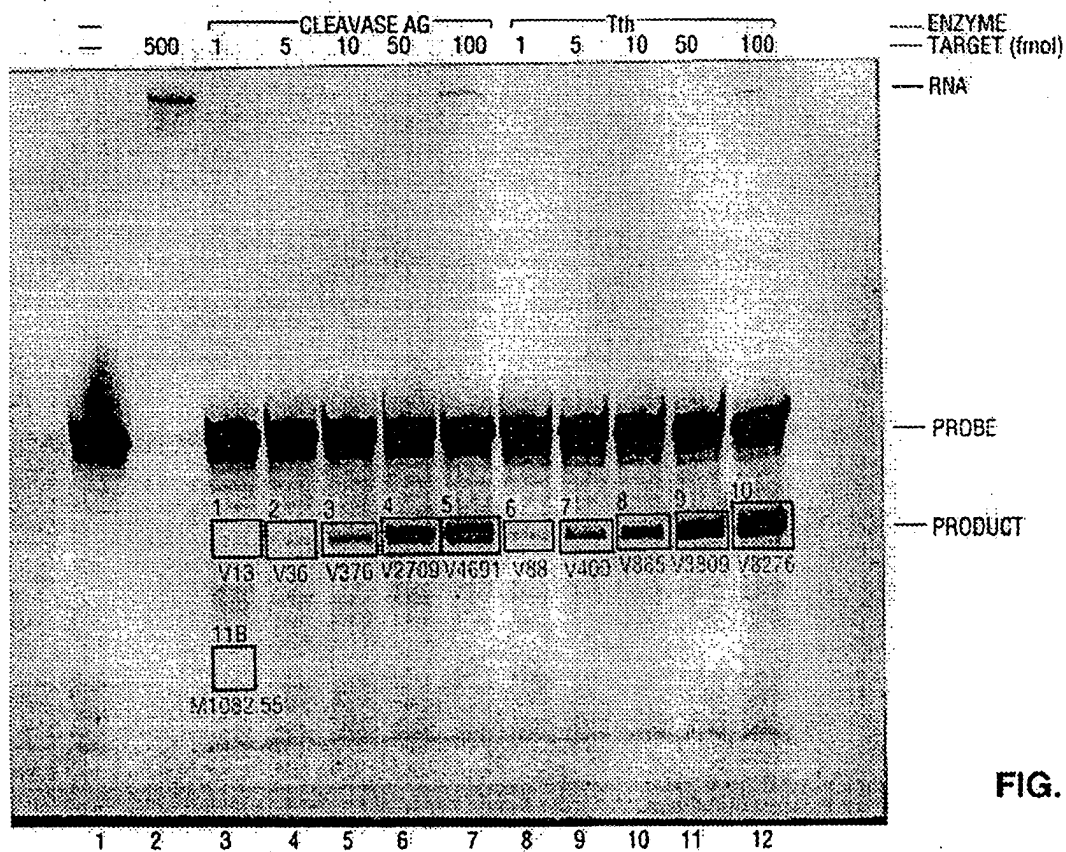
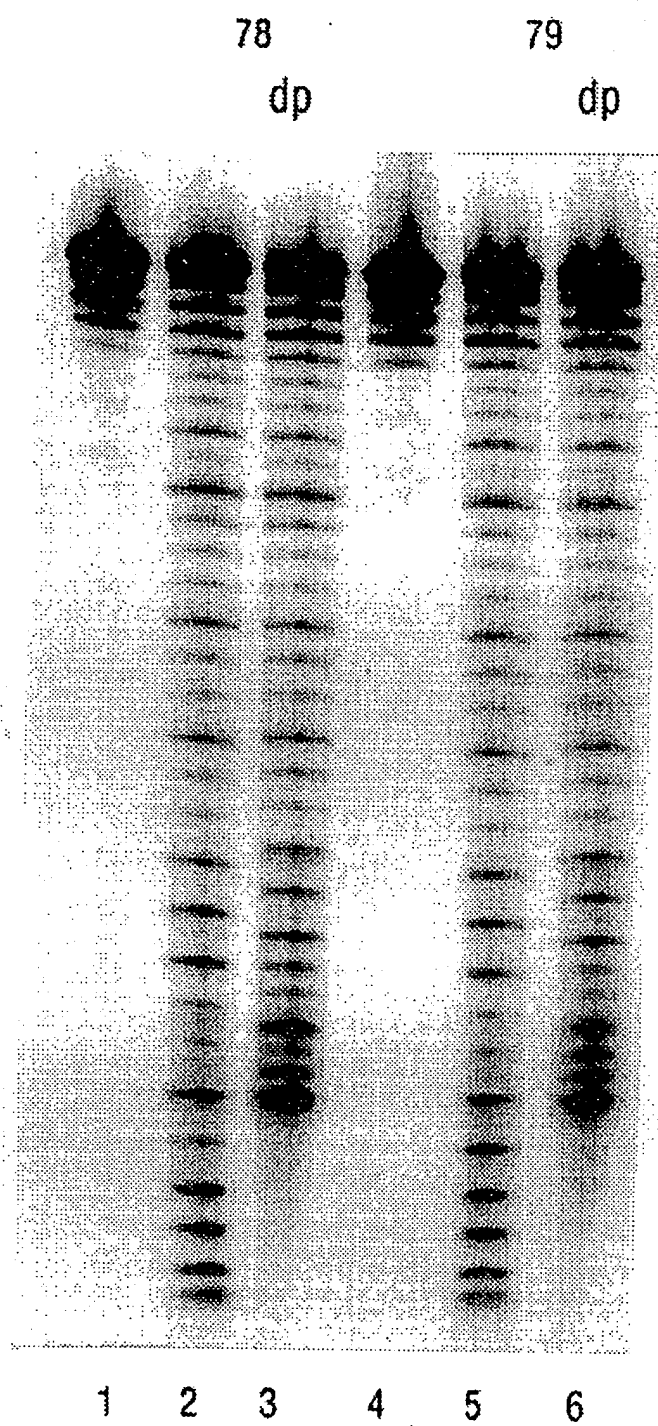


FIG. 54

**FIG. 55**

70 (C10 amino T's)  
74 (C6 amino T's)

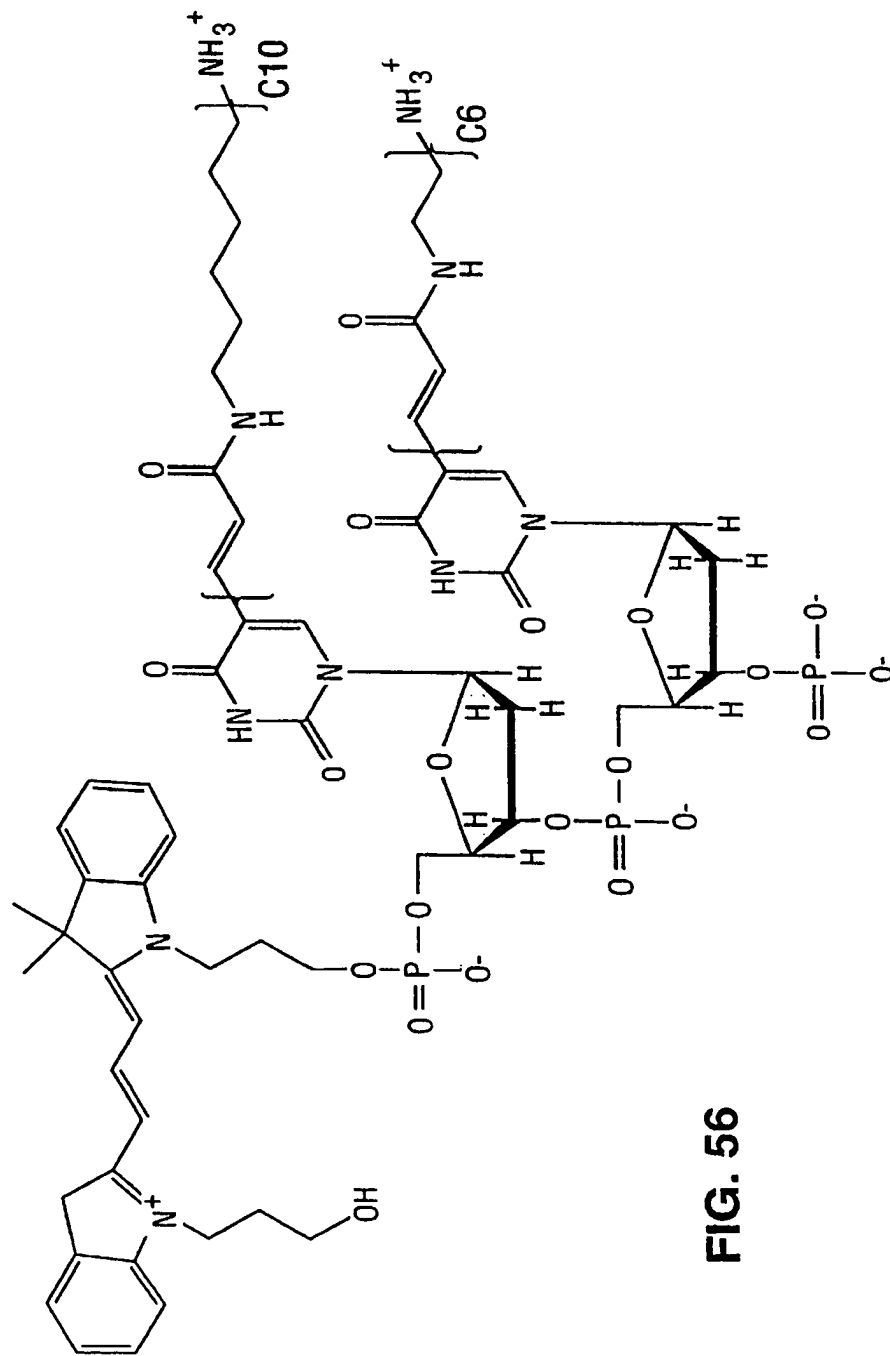


FIG. 56

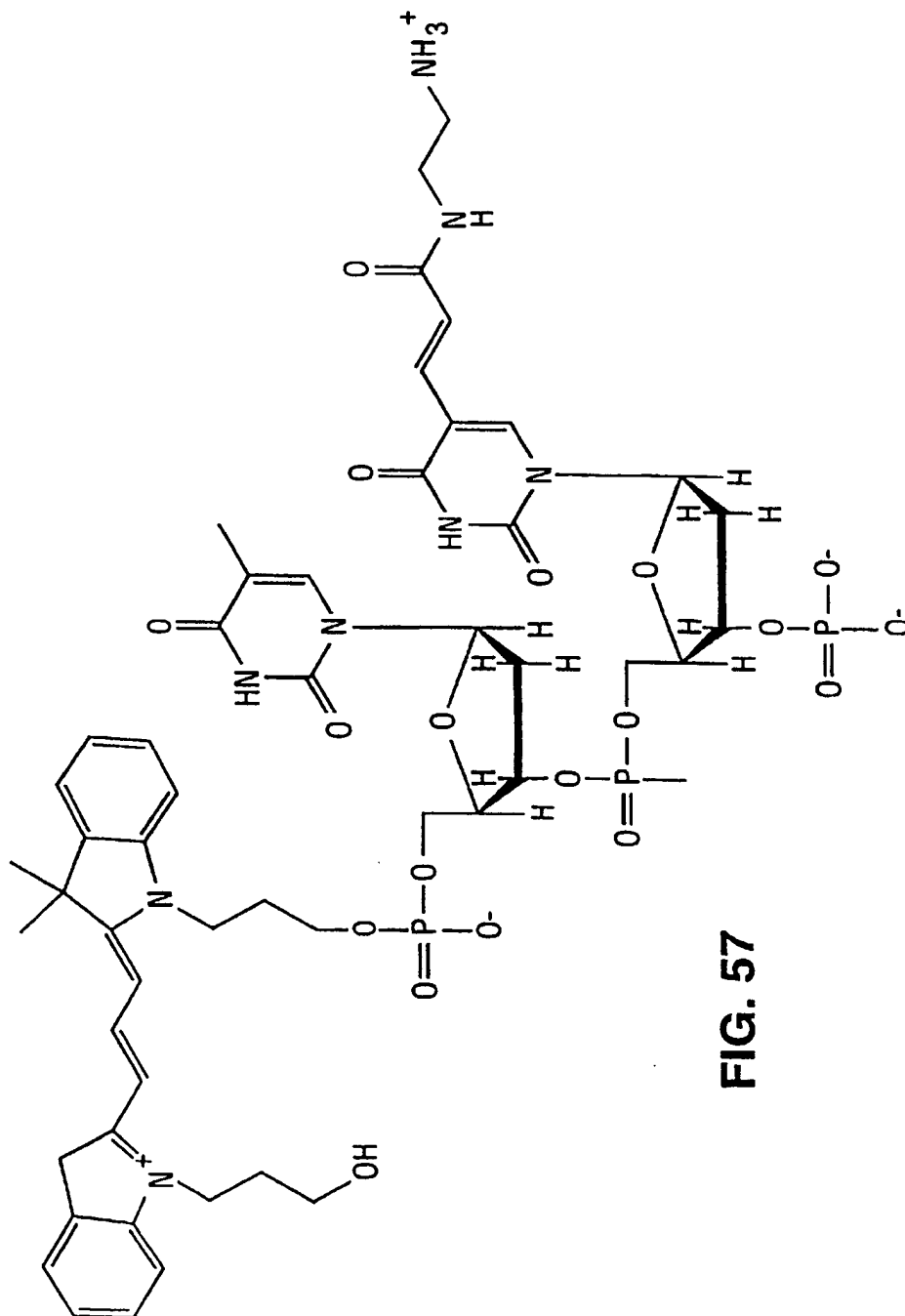


FIG. 57



76

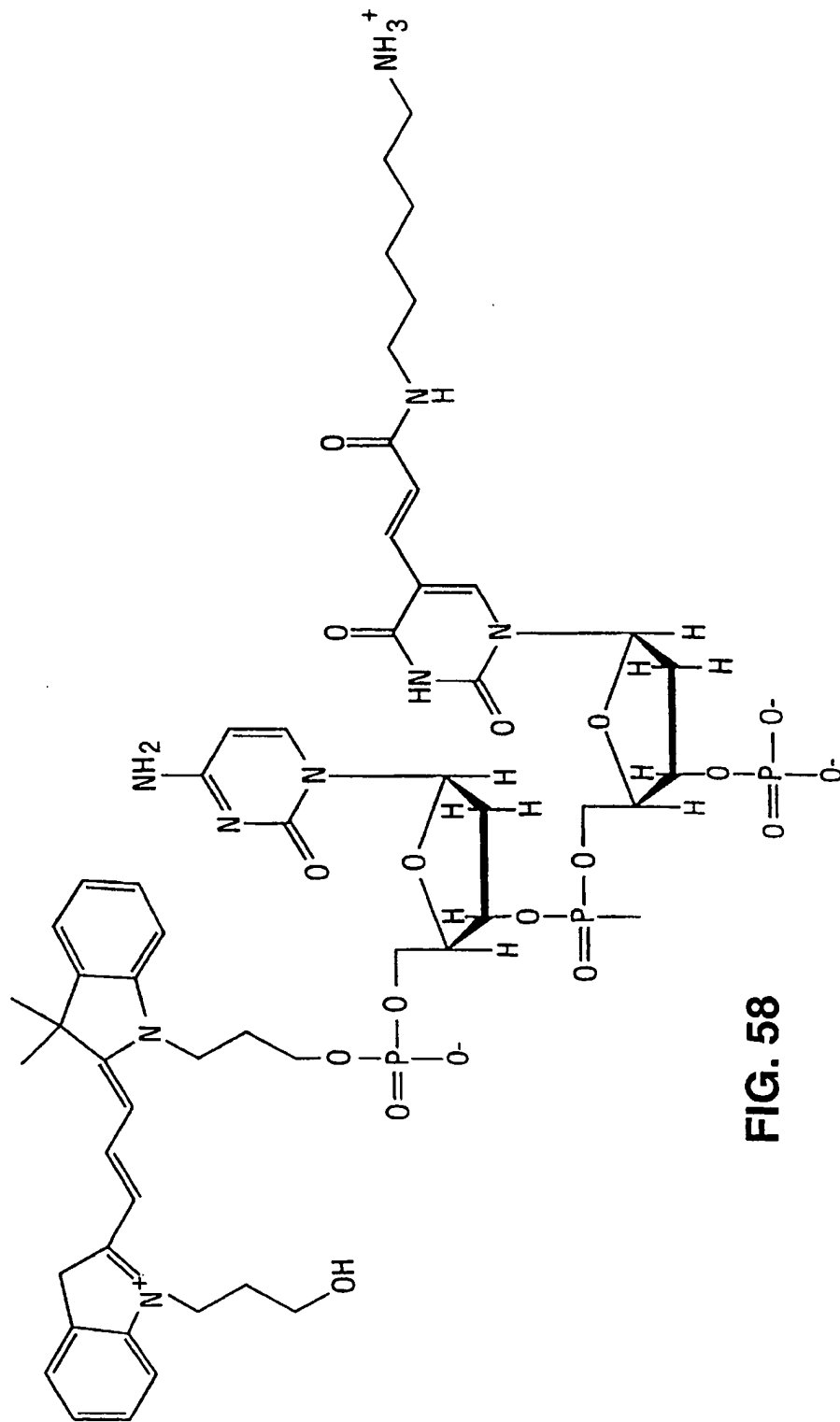
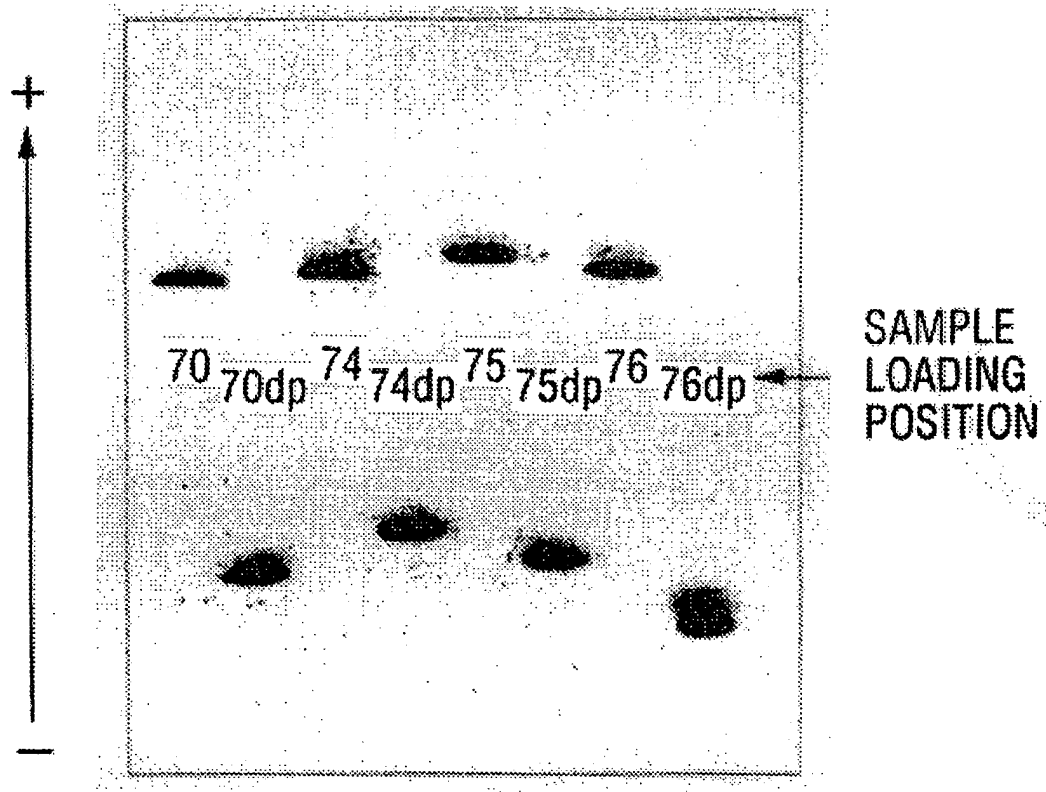
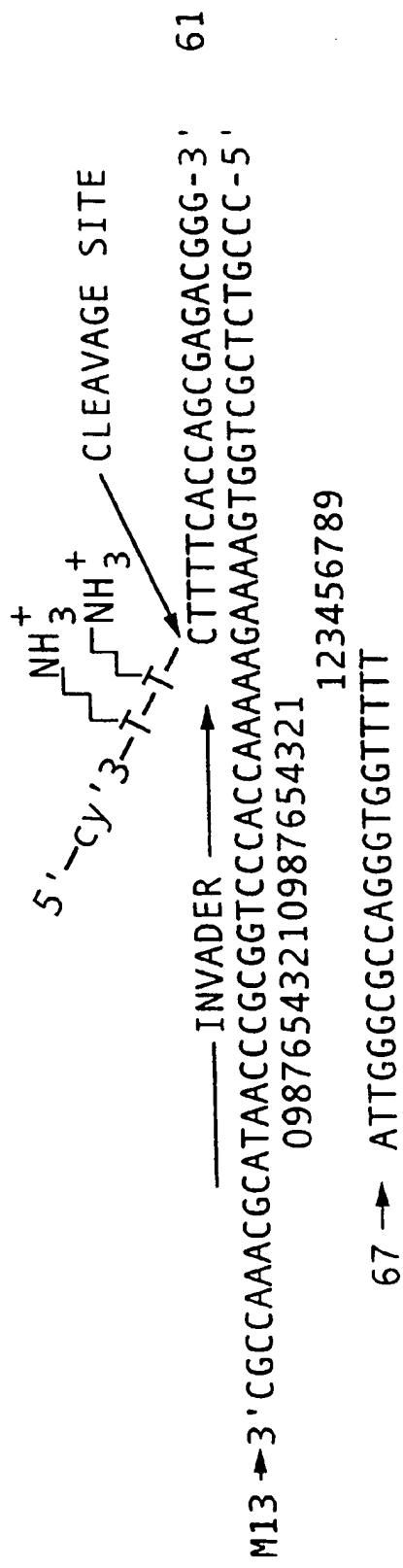


FIG. 58

**FIG. 59**



**FIG. 60A**

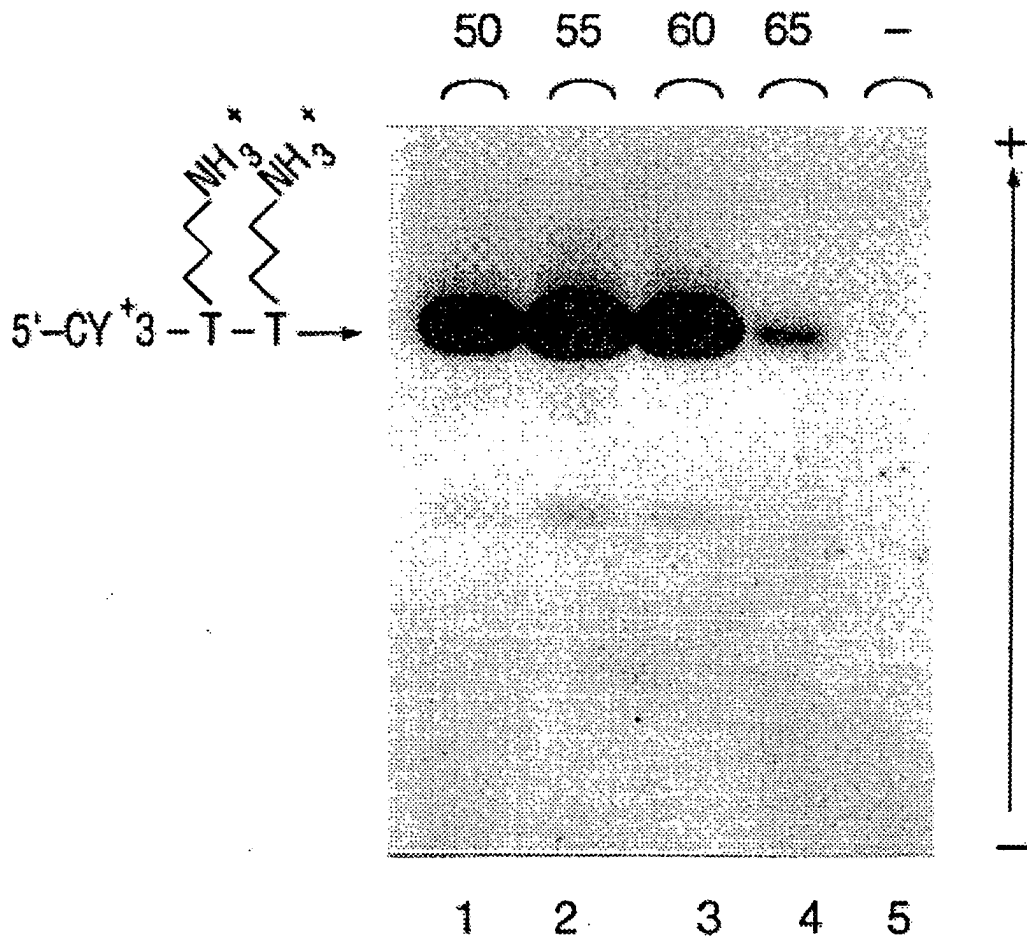


FIG. 60B

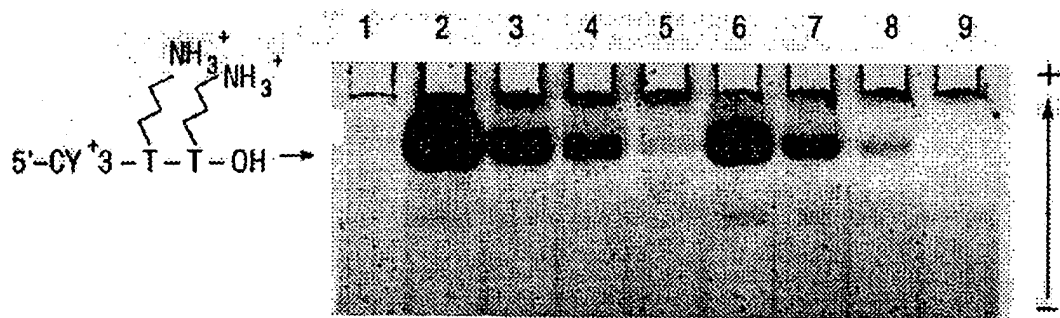


FIG. 61

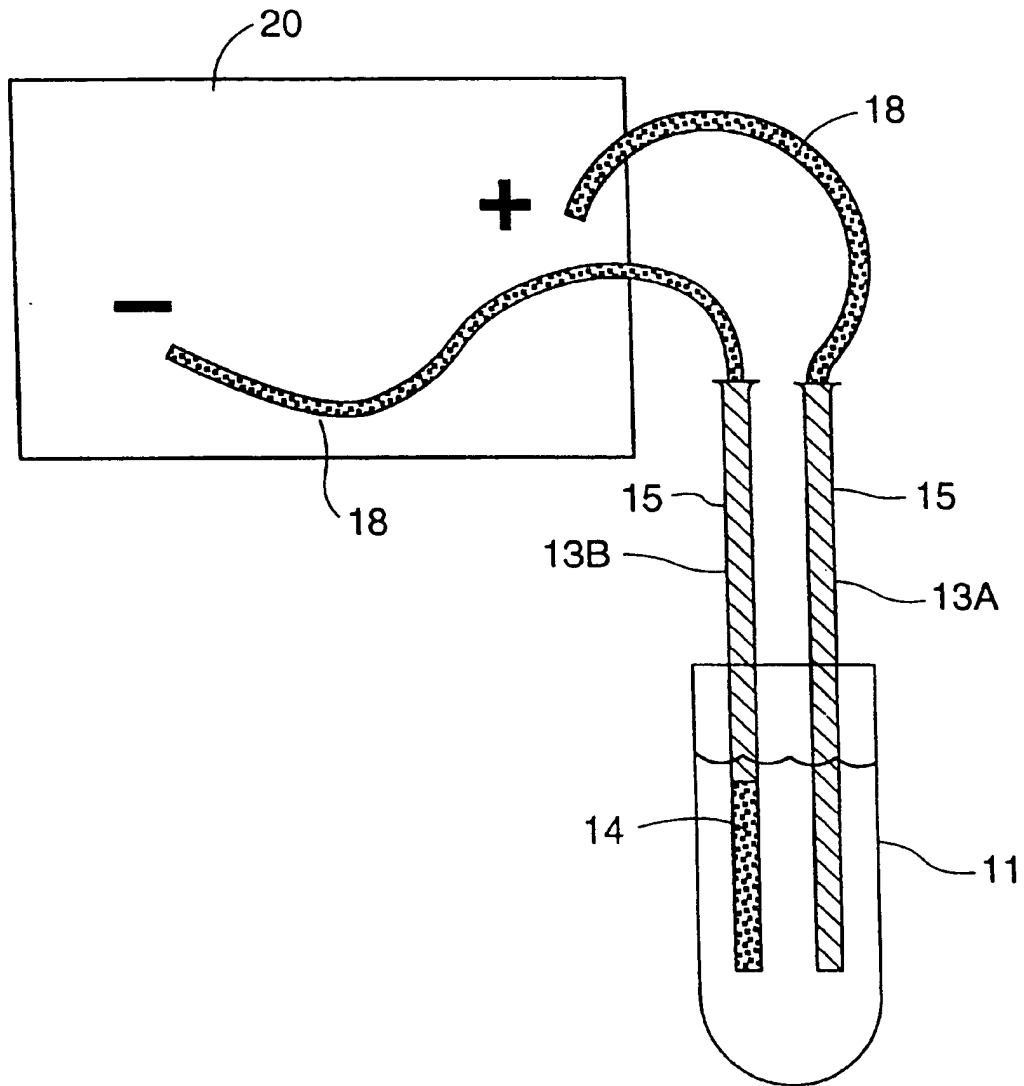


FIG. 62

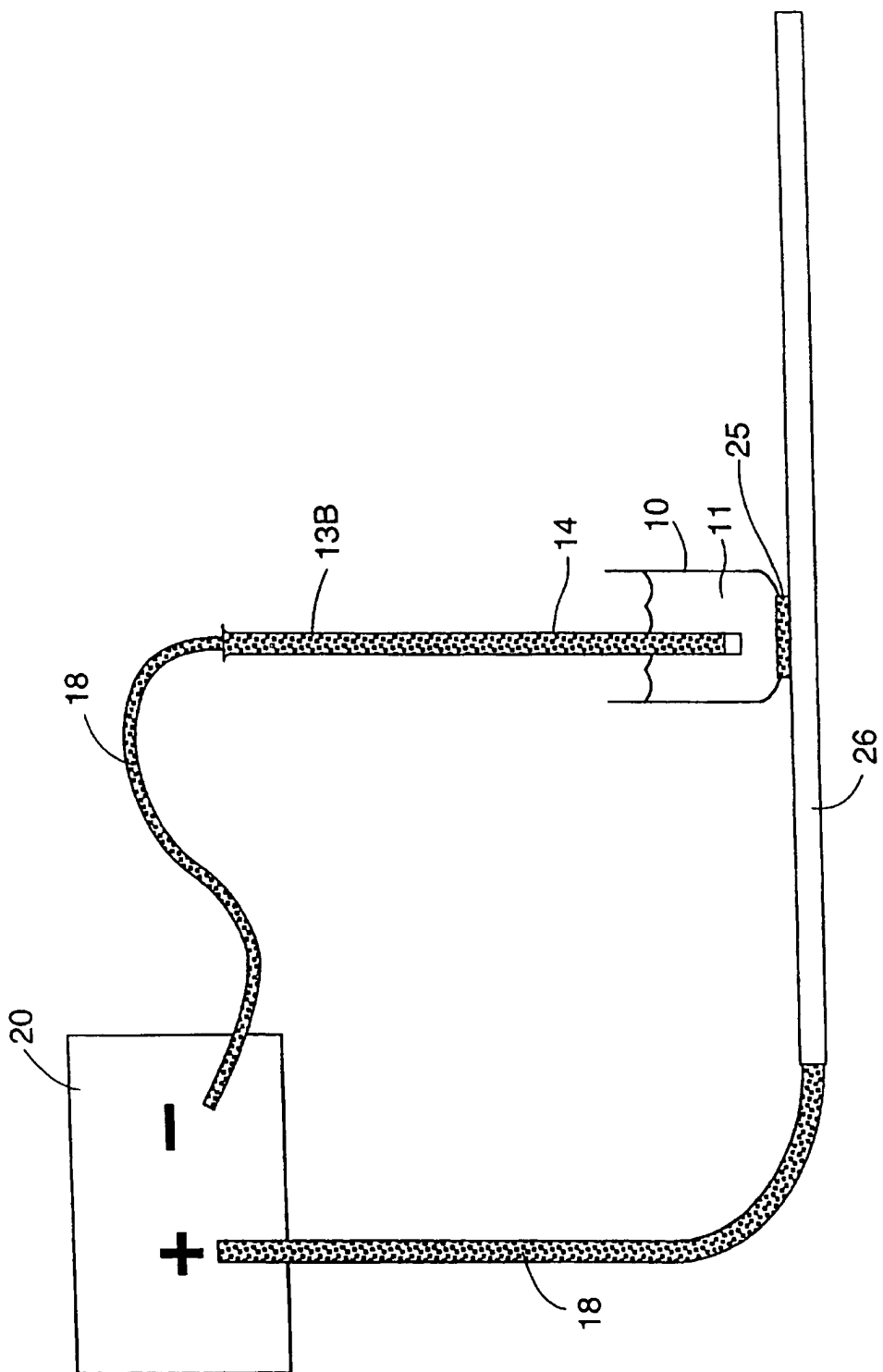


FIG. 63

PRIMER

- + C T A G

25 →

1 2 3 4 5 6

FIG. 64



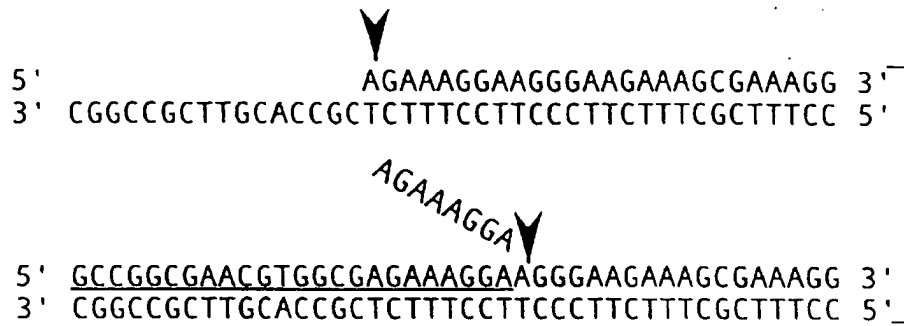


FIG. 65A



FIG. 65B



FIG. 65C



FIG. 65D

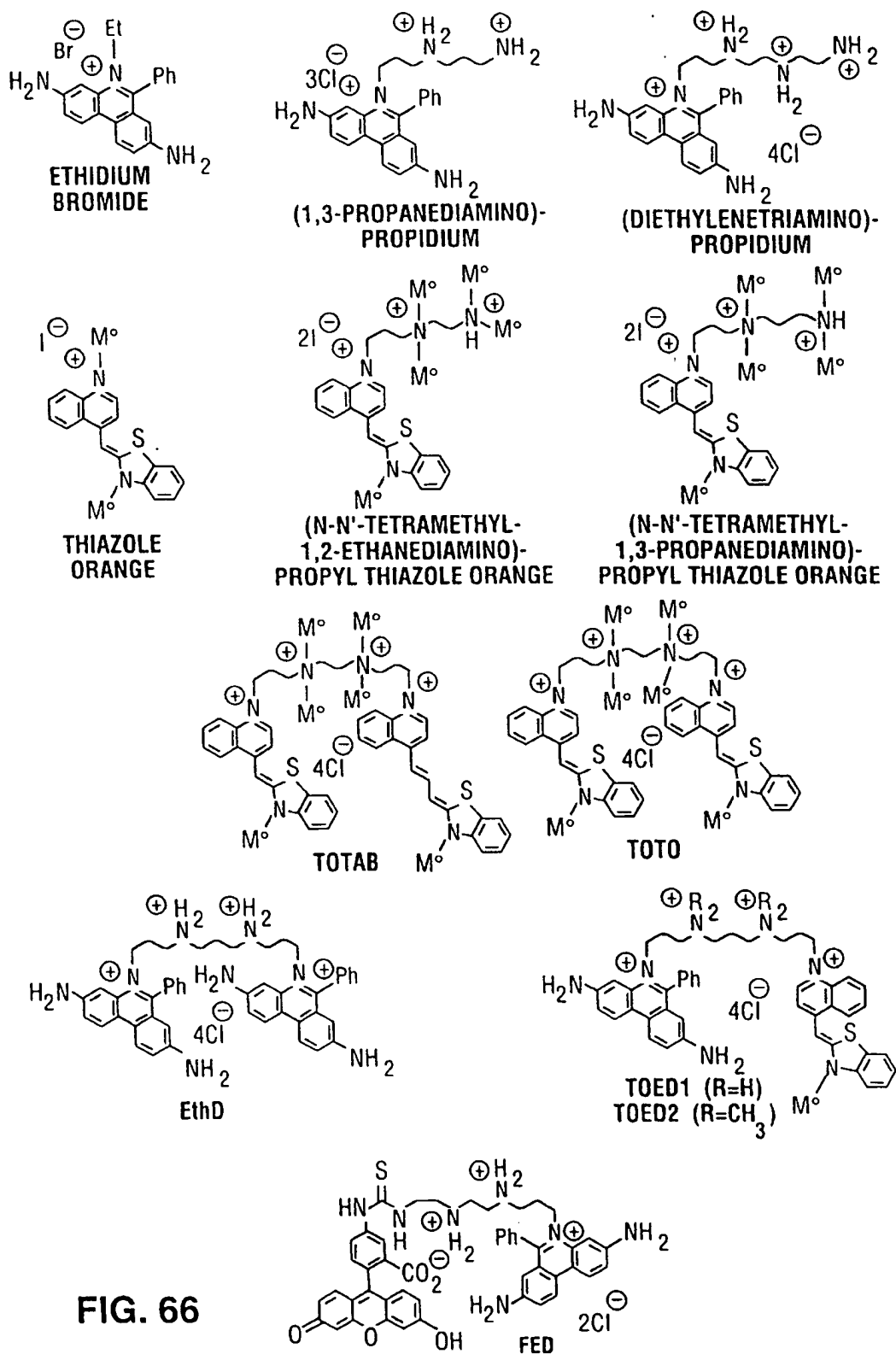


FIG. 66